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March 31, 2006, 06:58:31 ; Search time 15.3602 Seconds (without alignments) 10767.297 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
COLUMNICO	ID	US-09-925-065A-502888	US-10-027-632-166247	US-10-027-632-166247	US-09-925-065A-661036	US-09-925-065A-665667	US-10-613-053A-1	US-10-451-366A-1	US-09-835-232-6	US-10-308-485-6	US-10-195-144-87	US-10-345-072-87	US-09-925-065A-199410	US-09-925-065A-199411	US-10-027-632-155478	US-10-027-632-155478	US-10-630-518-17	US-10-630-518-21	US-09-925-065A-97366	US-09-925-065A-853310	US-09-925-065A-601207	US-09-925-065A-601208	US-10-087-192-1948	US-09-925-065A-192206
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	Score	19	19	19	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18	18	18	18	18	18	17.4	17.4	17.4	17.4	17.4	16.8
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Sequence 166247, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome

RESULT 2 US-10-027-632-166247/c

Sequence 192207, Sequence 63, Appl Sequence 580465, Sequence 642314, Sequence 642314, Sequence 642314, Sequence 747766, Sequence 317894, Sequence 317894, Sequence 317894, Sequence 38621, A Sequence 38621, A Sequence 38621, A Sequence 222608, Sequence 222608, Sequence 58881, Sequence 588814, Sequence 588834,	Single the Human Genome	gth 715; Indels 0; Gaps 0;
US-09-925-065A-192207 US-10-926-683-63 US-09-925-065A-580465 US-09-925-065A-642314 US-09-925-065A-642314 US-09-925-065A-642314 US-09-925-065A-642314 US-09-925-065A-642315 US-09-925-065A-642316 US-10-027-632-92083 US-10-027-632-92083 US-10-027-632-92083 US-10-027-632-9317894 US-10-027-632-9317894 US-10-027-632-9317894 US-10-027-632-9317894 US-10-027-632-9317894 US-10-027-632-9317894 US-10-027-632-9317894 US-09-925-065A-93621 US-09-925-065A-9363186 US-09-925-065A-222608 US-09-925-065A-22608 US-09-925-065A-2885834 US-09-925-065A-2885834 US-09-925-065A-2885836	JGNMENTS SS065A and Mapping of ymorphisms in 125,065A 1,096 2,147 1,092 1,766 1,846 10n 4.0	Score 19; DB 4; Len Pred. No. 6.2e+02; 0; Mismatches 0; 19
40044444444	c lication US/0 050228172A9 vid G. Identificati Muclectide 827.135 NUMBER: US/0 1200-10-24 UMBER: US 60/2000-11-20 UMBER: US 60/2000-11-20 UMBER: US 60/2000-11-30 UMBER: US 60/2000-11-30 UMBER: US 60/2000-11-30 UMBER: US 60/2001-01-16 UMBER: US 60/2001-01-16 UMBER: US 60/2001-01-16 UMBER: US 60/2001-01-16 UMBER: US 60/2001-05-09 S2 957086 or Windows Veriens	95.0%; 100.0%; ive TACAAAC
84.0 214 84.0 214 84.0 214 84.0 214 84.0 3.68 84.0 84.0 84.0 84.0 84.0 84.0 84.0 84.	ULT 1 09-925-065A-502888/C equence 502888/C equence 502888, Application US/0992 education No. US20050228172A9 ENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification TITLE OF INVENTION: Mucleotide Pol FILE REFERENCE: 108827.135 CURRENT PEPLICATION NUMBER: US/09/5CURRENT PEPLICATION NUMBER: US 60/245 PRIOR FILING DATE: 2000-11-20 PRIOR FILING DATE: 2000-11-20 PRIOR FILING DATE: 2000-11-30 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 957086 SOFTWARE: FASTSEQ for Windows Versi EQ ID NO 502888 LENGTH: 715 TYPE: DNA ORGANISM: Homo Sapiens	nilarity Conservat IGAATATATA I
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SULT 1  -09-925-065A-502888/c Sequence 50288, Appl Publication No. US200 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 1088: CURRENT APPLICATION UP PRIOR PILING DATE: 2 PRIOR APPLICATION NU PRIOR FILING DATE: 2 PRIOR APPLICATION NU PRIOR APPLICATION NU PRIOR FILING DATE: 2 PRIOR APPLICATION NU PRIOR APPLICATION NU PRIOR FILING DATE: 3 PRIOR APPLICATION NU PRIOR FILING DATE: 3 PRIOR APPLICATION NU PRIOR FILING DATE: 3 PRIOR PRIOR FILING DATE: 3 PRIOR PRIOR FILING DATE: 3 PRIOR	atch cal S 19
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                        441 TTGAATATATATTACAAAG 423
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Best Local Similarity 95.0
Matches 19; Conservative
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US-09-925-065A-661036
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US-09-925-065A-665667
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Sequence 166247, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108027.1532

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 166247
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Pred. No. 6.3e+02;
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100.0%; Pred. No. v...
0; Mismatches
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR PLILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1090-03-24

PRIOR FILING DATE: 1090-10-24

PRIOR FILING DATE: 1099-10-28

PRIOR PRIOR DATE: 1099-10-28

PRIOR APPLICATION NUMBER: US 60/156,368

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-09-09

PRIOR FILING DATE: 1999-09-09-09

PRIOR FILING DATE: 1999-09-09-09

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Best Local Similarity 100.
Matches 19; Conservative
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ORGANISM: Human
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LENGTH: 819
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ITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PAPLICATION NUMBER: US 60/250,092
PRIOR PAPLICATION NUMBER: US 60/261,766
PRIOR PAPLICATION NUMBER: US 60/269,846
PRIOR PILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
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Query Match 92.0%; Score 18.4; DB 3; Length 180216; Best Local Similarity 95.0%; Pred. No. 1.5e+03; Matches 19; Conservative 0; Mismatches 1; Indels 0;
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| Sequence 6, Application US/09835232 |
| Sequence 6, Application US/09835232 |
| Sequence 6, Application US/09835232 |
| SERENAL INFORMATION |
| APPLICANT: Leder, Philip |
| APPLICANT: Leder, Benjamin |
| TILE OF INVENTION | FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES |
| TILE OF INVENTION | FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES |
| TILE OF INVENTION | FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES |
| TILE OF INVENTION | STATES |
| CURRENT PRILING DATE: 2001-04-12 |
| PRIOR APPLICATION NUMBER: US 60/196,811 |
| PRIOR FILING DATE: 2000-04-13 |
| PRIOR PRINCE DATE: 2000-04-13 |
| PRIOR P
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 180216
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4150 TTGAATATATATAAAAGC 4131
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; LOCATION: (1)...(180216)

; OTHER INFORMATION: n = A,T,C or G

US-09-835-232-6
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; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6
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ORGANISM: Homo sapiens
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APPLICANT: SAKAI, Takako
APPLICANT: SOLOMO, Hideya
APPLICANT: KOIZUKA, Nobuya
APPLICANT: HAYAKAMA, Takahiko
TITLE OF INVENTION: A Protein Which is Involved in Recovery of Cytoplasm Male
TITLE OF INVENTION: Fertility from Sterility and a Gene Encoding the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10451366A
Publication No. US20040117868A1
GENERAL INFORMATION:
APPLICANT: IMAMURA, Jun
APPLICANT: SAKAI, Takako
APPLICANT: ROIZUKA, Nobuya
APPLICANT: ROIZUKA, Takahiko
APPLICANT: HAYAKAWA, Takahiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: P23889
CURRENT APPLICATION NUMBER: US/10/613,053A
CURRENT FILING DATE: 2003-07-07
PRIOR APPLICATION NUMBER: PCT JP02/04092
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/451,366A
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: PCT JP02/04092
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
ERQ ID NO 1
LENGTH: 8553
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US-10-613-053A-1/c
; Sequence 1, Application US/10613053A
; Publication No. US20040088749A1
                                                                           317 TTGAAATATATTACAAAGC 336
                           TIGAATATATATACAAAGC 20
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Best Local Similarity 95.04
Matches 19; Conservative
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ORGANISM: Raphanus sativus
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Best Local Similarity 95.0°
Matches 19; Conservative
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APPLICANT: IMAMURA, Jun
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US-10-345-072-87
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                                                                  APPLICANT: BROWN, GREGORY G.
APPLICANT: BROWN, GREGORY G.
APPLICANT: BROWN, MATASA
APPLICANT: BROWN, GREGORY G.
APPLICANT: GANDY, CHARLES
APPLICANT: CHEUNG, WING
APPLICANT: CHEUNG, WING
TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 16313-0136
CURRENT PILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/305,026
PRIOR APPLICATION NUMBER: 60/305,363
PRIOR APPLICATION NUMBER: 60/305,363
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ 1D NOS: 128
SOFTWARE PRECEDIAL VET. 2.1
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APPLICANT: LAI, FANG MING
APPLICANT: LAI, FANG MING
TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 16313-0210
CURRENT APPLICATION NUMBER: US/10/345,072
CURRENT PILING DATE: 2003-01-16
PRIOR FILING DATE: 2002-07-12
PRIOR PELLOR OF PRESENCE: 60/305,026
PRIOR APPLICATION NUMBER: 60/305,026
PRIOR APPLICATION NUMBER: 60/305,036
PRIOR APPLICATION NUMBER: 60/305,363
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PALCHING DATE: 2001-07-30
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LOCATTON: (144241)...(144300)

OTHER INFORMATION: a, t, c, g, other or unknown

US-10-195-144-87
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Publication No. US20030237112A1
GENERAL INFORMATION:
APPLICANT: BROWN, GREGORY G.
APPLICANT: FORMANOVA, NATASA
APPLICANT: DENDY, CHARLES
APPLICANT: CANDRY, BENOIT S.
APPLICANT: CHEUNG, WING
; Sequence 87, Application US/10195144; Publication No. US20030126646A1; GENERAL INFORMATION;
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Matches 19; Conservative
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ORGANISM: Raphanus sativum
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Publication No. US20050228172A9

GENERAL INPORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

FRIOR PRILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-05-09

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SEQ ID NO 199410

LENGTARE: PASSED FOR WINDOWS VERSION 4.0

LENGTH: 372
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Fublication No. US2050228172A9
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-20
FRIOR PRICATION NUMBER: US 60/250,092
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SEQ ID NO 87
LENGTH: 271990
TYPE: DNA
ORGANISM: Raphanus sativum
PERATURE:
NAME/KEY: modified base
LOCATION: (144241)...(144300)
OTHER INFORMATION: a, t, c, g, other or unknown
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Best Local Similarity 95.09
Matches 19; Conservative
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US-09-925-065A-199410
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US-09-925-065A-199411/c
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CURRENT APPLICATION NUMBER: US/10/027,632
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION MUMBER: US/10/027,632

CURRENT PAPLICATION NUMBER: US/60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARRE: FastSEQ for Windows Version 4.0
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; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.128
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                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 18; DB 4; Length 372; 100.0%; Pred. No. 1.5e+03; Live 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FestSEQ for Windows Version 4.0
SEQ ID NO 199411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 155478, Application US/10027632 Publication No. US20020198371A1
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Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-09-925-065A-199411
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US-10-027-632-155478
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CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SEQ TYMARE: FRAESEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 18, Conservative
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March 31, 2006, 07:14:39 ; Search time 11.0903 Seconds (without alignments) 7200.876 Million cell updates/sec
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2: $IDDSS/ptodata/2/pubpna/USO8 NEW PUB.seq:*

3: $IDDSS/ptodata/2/pubpna/USO7 NEW PUB.seq:*

4: $IDSS/ptodata/2/pubpna/PCT_NEW PUB.seq:*

5: $IDSS/ptodata/2/pubpna/USO9_NEW PUB.seq:*

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8: $IDDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*

10: $IDDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*

11: $IDDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*

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12: $IDDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*

13: $IDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*

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15: $IDDSS/ptodata/2/pubpna/USO0_NEW PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                          1 ttgaatatatattacaaagc 20
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Maximum DB seq length: 2000000000
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20
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 2, Appli Sequence 50.88, Sequence 60.38, Sequence 66.136, Sequence 66.767, Sequence 60.7861, Sequence 1221270, Sequence 288106, Sequence 199411, Sequence 97366, A Sequence 198305, Sequence 811714, Sequence 288107, Sequence 901515, Sequence 901516, Sequence 199410, Sequence 552100 Sequence 853310, Description US-09-925-065A-502888 US-09-925-065A-661036 US-09-925-065A-661036 US-09-925-065A-661036 US-10-301-480-607861 US-10-301-480-1221270 US-10-301-480-288106 US-10-301-480-288107 US-09-925-065A-199410 US-09-925-065A-199411 US-09-925-065A-97366 US-10-301-480-198305 US-09-925-065A-853310 US-10-301-480-552100 US-10-301-480-811714 000000 Query Match Length DB Score 18.4 18.4 18.4 18.4 18 18 18 18 18 17.4 17.4 17.4 17.4 Result g

Sequence 1165509, Sequence 601207, Sequence 601208, Sequence 39609, A Sequence 39609, A Sequence 6745, Ap	0916, 20, Ap 89, Ap 92206, 22207, 281767	Sequence 895177, Sequence 491022, Sequence 1054431, Sequence 371009, Sequence 580465,	
10 US-10-301-480-1165509 6 US-09-925-065A-601207 6 US-09-925-065A-601208 8 US-10-750-185-39609 8 US-10-750-623-39609 14 US-11-136-527-6745 14 US-11-136-527-2649	B US-10-750-185-60916 B US-10-750-623-60916 14 US-11-121-086-20 6 US-09-925-065A-192206 6 US-09-925-065A-192207 10 US-10-301-480-895,75	10 US-10-301-480-281768 110 US-10-301-480-895177 10 US-10-301-480-441022 10 US-10-301-480-1054431 6 US-09-925-065A-371009 6 US-09-925-665A-580465 6 US-09-925-665A-8112	6 US-09-925-065A-642314 6 US-09-925-065A-642315 6 US-09-925-065A-642316 6 US-09-925-065A-747766 6 US-09-925-065A-797645
595 596 596 1294 1400 1653	2866 2866 162289 165627 211 211 212	218 218 351 352 368 417	417 417 417 458
87.0 87.0 87.0 87.0 87.0	87.0 87.0 87.0 84.0 84.0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	84.0 84.0 84.0 84.0
1,71 1,71 1,71 1,71 1,71 1,71 1,71 1,71	17.7.1 17.7.4 16.8 16.8 16.8 16.8	110000000000000000000000000000000000000	16.8 16.8 16.8 16.8
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## ALIGNMENTS

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APPLICANT: Martens, Amy
APPLICANT: Sammons, Bernard
TITLE OF INVENTION: Cotton Event MON 88913 and Compositions and Methods for Detection
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Chimeric DNA of cotton genomic DNA and transgene insert DNA
US-10-541-346-2
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Pred. No. 23;
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100.0%; Pred. No. 2...
... 0; Mismatches
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/541,346
CURRENT APPLICATION NUMBER: US/10/541,346
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: 60/447,184
PRIOR FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
LENGTH: 20
              Sequence 2, Application US/10541346
Publication No. US20060059590A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTGAATATATATACAAAGC 20
                                                                          APPLICANT: Cerney, Eric
APPLICANT: Duong, Can
APPLICANT: Hart, Jesse
APPLICANT: Huber, Scott
APPLICANT: Krieb, Rachel
APPLICANT: Listello, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                   Publication No. US20060059590A1
GENERAL INFORMATION:
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Watches 20; Conservative
JS-10-541-346-2
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RESULT 2 US-10-541-346-4

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Sequence 661036, Application US/09925065A

Publication No. US20040181048A1

SEQUENCE 661036, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE REFERENCE: 108027.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR FILING DATE: 2001-01-16

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Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-01-16
PRIOR PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASICES for Windows Version 4.0
SEQ ID NO 665667
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US-09-925-065A-661036
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US-09-925-065A-665667
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TITLE OF INVENTION: Coctron Event MON 88913 and Compositions and Methods for Detection
TITLE OF INVENTION: Thereof
FILE REFERENCE: 11899.0239.PCUS00
CURRENT APPLICATION NUMBER: US/10/541,346
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: 60/447,184
PRIOR APPLICATION NUMBER: 60/447,184
SPRIOR APPLICATION NUMBER: 60/447,184
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Chimeric DNA of cotton genomic DNA and transgene insert DNA US-10-541-346-4
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i Sequence 50288, Application US/09925065A

j Sequence 50288, Application US/09925065A

j Sequence 50288, Application US/09925065A

j GENERAL INFORMATION:
    TITLE OF INVENTION: Identification and Mapping of Single
    TITLE OF INVENTION: Identification and Mapping of Single
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    TITLE OF INVENTION: NUMBER: US/09/925,065A

    CURRENT APPLICATION NUMBER: US 60/243,096

    PRIOR FILING DATE: 2000-10-24

    PRIOR APPLICATION NUMBER: US 60/250,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2000-11-16

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR
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100.0%; Score 20; DB 10; Length 1675;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 20; Conservative 0; Mismatches 0; Indels 0
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    Application US/10541346
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                                                                                                                           APPLICANT: Cerney, Eric
APPLICANT: Duong, Can
APPLICANT: Hart, Jesse
APPLICANT: Huber, Scott
APPLICANT: Krieb, Rachel
APPLICANT: Listello, Jennifer
APPLICANT: Martens, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
Sequence 4, Application US/1054
Publication No. US20060059590A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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US-09-925-065A-502888
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Matches 19; Conserv
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LENGTH: 1675
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APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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Length 607; Indels ö

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441 TTGAATATATATTACAAAG 423

Gaps

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US,10/301,480
CURRENT PELING DATE: 2002-11-21
PRIOR FILING DATE: 2002-18-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PASESEQ for Windows Version 4.0
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: in the Human Genome
FILE SPERMENCE: 108827.137
CURRENT PRILICATION NUMBER: US/10/301,480
CURRENT PILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/211,695
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSRQ for Windows Version 4.0
SEQ ID NO 288107
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| Sequence 901515, Application US/10301480
| Publication No. US20060057564A1
| Sequence 901515, Application No. US20060057564A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. | TITLE OF INVENTION: In the Human Genome | TITLE OF INVENTION: In the Human Genome | FILE REPERENCE: 108827.137 | CURRENT APPLICATION NUMBER: US/10/301,480 | CURRENT APPLICATION NUMBER: US | 10/215,598 | PRIOR APPLICATION NUMBER: US | 10/215,598 | PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 369; 3.2e+02;
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100.0%; Pred. No. s...
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100.0%; Pre
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapien
US-10-301-480-288106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapien
US-10-301-480-288107
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hes 18; Conserv
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  GENERAL INFORMATION:
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Best Local S
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                                                                                                                                       Sequence 607861, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: PRASESQ for Windows Version 4.0
; SEQ ID NO 607861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1221270, Application US/10301480

Sequence 1221270, Application US/10301480

Publication No. US2006005564A1

GENERAL INFORMATION:

APPLICATIN WANG, DAVIG G.

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

FILE REPERENCE: 10827.137

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-09-09

PRIOR PILING DATE: 2002-09-09

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 1221270

LENGTH: 789
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US-10-301-480-288106/c
; Sequence 288106, Application US/10301480
; Publication No. US20060057564A1
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1 TTGAATATATATACAAAGC 20
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Matches 19; Conservative
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US-10-301-480-1221270
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ORGANISM: Homo sapien
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US-10-301-480-1221270/c
                                                                                                                           US-10-301-480-607861/c
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Gaps

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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 199410
; LENGTH: 372
; LENGTH: 372
; YPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199410
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100.0%; Pre-
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Matches 18; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-199411
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US-09-925-065A-199411/c
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Sequence 901516, Application US/10301480

Publication No. US2060057564A1

GENERAL INFORMATION:
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
TILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR PILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 901516
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Sequence 199410, Application US/09925065A

PUBLICAUTON

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Naclectide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2001-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086
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100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.2e+02;
cive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
ERQ ID NO 901515
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Best Local Similarity 100.C
Matches 18; Conservative
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Matches 18; Conservative
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US-10-301-480-901515
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US-10-301-480-901516
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GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/260,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTERQ for Windows Version 4.0
SEQ ID NO 199411
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FUBLICATION NO. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-11-20
FRIOR PAPLICATION NUMBER: US 60/251,47
FRIOR FILING DATE: 2000-11-20
FRIOR PAPLICATION NUMBER: US 60/250,092
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FRIOR PAPLICATION NUMBER: US 60/250,092
FRIOR FILING DATE: 2000-11-30
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Length 372;
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Query Match 90.0%; Score 18; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 198305, Application US/10301480

Sequence 198305, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: 10827.137

CURRENT FILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SEQ ID NOS: 1226818

LENGTH: 553
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87.0%; Score 17.4; DB 6; Length 546;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97366
LENGTH: 546
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Best Local Similarity 94.7°
Matches 18; Conservative
                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-925-065A-97366
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CORGANISM: Homo sapien
US-10-301-480-198305
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                                                                                                                                TYPE: DNA
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Sequence 27,
Sequence 27,
Sequence 6, A
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Sequence 28,
Sequence 27,
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Sequence 11,
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Sequence 9,
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-09-737-626A-28

US-10-427-180-28

US-09-737-698B-27

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US-09-737-626A-27

US-09-737-626A-27

US-10-427-180-27

US-10-427-180-27

US-08-366-26-44

US-07-809-457A-17

US-08-466-06-11

US-08-466-06-11

US-08-803-97-99

US-08-803-97-99

US-08-803-97-99

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US-08-933-485-11

US-09-117-440-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                nucleic search, using sw model
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seq length: 200000000
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Perfect score:
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LOCATION: (1)..(1695)

OTHER INFORMATION: n=a or g or c or t/u, r=g or a, y=t/u or c

OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intra
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| Patent No. 646228
| GENERAL INFORMATION:
| APPLICANT: FINCHER, Karen
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: No. 646228el Plant Expression Constructs
| TITLE OF INVENTION: No. 646228el Plant Expression Constructs
| FILE REFERENCE: 38-21(14.99)C
| CURRENT APPLICATION NUMBER: US/09/737,698B
| CURRENT FILING DATE: 2000-12-15
| PRIOR PILING DATE: 1999-12-16
| NUMBER OF SEQ ID NOS: 30
| SEQ ID NO 28
| LENGTH: 1695
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PCT-US91-09437-17

US-09-134-0378-27

US-09-434-0338-27

US-09-434-0338-27

US-09-434-0398-31

US-09-434-0398-29

US-09-434-0398-32

US-09-434-0398-32

US-09-434-0398-32

US-09-434-0398-3

US-09-182-117-1

US-09-182-117-4

US-09-182-117-5

US-09-182-117-5

US-09-182-117-5

US-09-182-117-5
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  NAME/KEY: promoter
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NAME/KEY: promoter
LOCATION: (1)..(1695)
OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro-
US-10-427-169-28
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; Sequence 28, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
    APPLICANT: Flaciner, Stanislaw
; APPLICANT: Flashiski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 691949561 Plant Expression Constructs
; TITLE OF INVENTION: No. 691949561 Plant Expression Constructs
; FILE REFERENCE: 38-21 (51499) B
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-02-25
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LANCE TO A SEC ID NOS: 30
; SEQ ID NO 28
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Best Local Similarity
Matches 646; Conserva'
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CTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c

CTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intrd
US-09-737-626A-28
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                                                                                                      301 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAAGAGCTGTCCTGACAGCC
                                                                                                                                                                       361 CACTCACTAATGCGTATGACGAACGCAGTGACGACCACAAAAGAATTAGCTTGAGCTCAG
                                                                                                                                                                                                                               2655 GATTTAGCAGCATTCCAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTC
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| Sequence 28, Application US/09737626A
| Patent No. 6660911
| SEMERAL INFORMATION:
| APPLICANT: Fincher, Karen
| APPLICANT: Flasinski, Stanislaw
| APPLICANT: Wilkinson, Jack
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
| FILE REFERENCE: 38-21(51499)B
| CURRENT PILING DATE: 2002-225
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR PELING DATE: 2000-12-15
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: artificial sequence
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-09-737-626A-28
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NAME/KEY: promoter

LOCATION: (1)..(1946)

. OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +

. OTHER INFORMATION: ntro

US-09-737-698B-27
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19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred. No. 9.4e-111;
Matches 548; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)
CURRENT PRILOATION NUMBER: US/09/737,698B
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,173
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09737698B; Patent No. 6462258; GENERAL INFORMATION:
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US-09-737-698B-27
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OTHER INFORMATION: n=a or g or c or c or c or a, y=c or c or c
OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro
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Fatent No. 6949696
GENERAL INCOMATION
APPLICANT: Flucher, Karen
APPLICANT: Flatinski, Stanislaw
APPLICANT: Wilkinson, Jack
TILE OF INVENTION NO. 69496961 Plant Expression Constructs
FILE REFERENCE: 38-21(51499)8
CURRENT APPLICATION NUMBER: US/09/737,626
FRIOR PILING DATE: 2003-05-01
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-02-25
PRIOR PLING DATE: 2003-02-25
PRIOR PLING DATE: 2003-02-25
SPIOR PLING DATE: 2003-02-25
SPIOR PLING DATE: 2003-02-15
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH 1695
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; LUCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Actll polynucleotides + Actll
; OTHER INFORMATION: ntro
US-10-427-169-27
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| Sequence 27. Application US/10427169
| Patent NO. 6919495
| GENERAL INFORMATION:
| APPLICANT: Flincher, Karen
| APPLICANT: Flincher, Stanislaw
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: No. 691949561 Plant Expression Constructs
| TILE REFERENCE: 38-21(51499) B. CURRENT APPLICATION NUMBER: US/10/427,169
| CURRENT FILING DATE: 2003-05-01
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR PRING DATE: 2000-12-15
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 27
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ilarity 100.0%; Pred. No. 9.4e-111;
Conservative 0; Mismatches 0;
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ORGANISM: artificial sequence
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Best Local Simi
Matches 548;
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US-10-427-169-27
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NAME/KEY: promoter

LOCATION: (1). (1946)

COTHER INFORMATION: chimeric promoter fusion FMV and Actil polynucleotides + Actil

OTHER INFORMATION: ntro

US-09-737-626A-27
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US-09-737-626A-27
; Sequence 27, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Fincher, Karen
; APPLICANT: Wilkinson, Jack
; TILE OF INVENTYON: No. 6660911el Plant Expression Constructs
; TILE OF INVENTYON: No. 6660911el Plant Expression Constructs
; TILE OF INVENTYON: NO. 6660911el Plant Expression Constructs
; TILE NOT INVENTY PRILICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Version 3.0
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19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred. No. 9.4e-111;
Matches 548; Conservative 0; Mismatches 0; Indels
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LENGTH: 1946
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CACTCACTAATGCGTATGACGAACGCAGTGACGACCACAAAAGAATTAGCTTGAGCTCAG
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    Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,738B
FILING DATE: 19910903
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HOGENET J. Dennis R.
REGISTRATION NUMBER: 30,914
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10536)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lawson, Edgar C.
APPLICANT: Lawson, Edgar C.
APPLICANT: Hemenway, Cynthia L.
APPLICANT: Hemenway, Cynthia L.
APPLICANT: Tumer, Nilgun B.
TITLE OF INVENTION: Virus Resistant Plants and Met.
TITLE OF INVENTION: Therefore
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis R. Hoerner, Jr., Monsanto Co. B
STREET: ALOUGH CLESTERIFIED OF CONTRANTS: USA
CITY: St. Louis
STATE: Missouri
CONNTRY: USA
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Patent No. 5304730
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OTHER INFORMATION: chimeric promoter fusion FWV and Actil polynucleotides
OTHER INFORMATION: ntro
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    AATTCTCAGTCCAAAGCCTCAACAAGGTCAGGGTACAGAGTCTCCAAACCATTAGCCAAA
                                               2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAGTAAACTACTGTTCCAGCACATGCA
                                                                         AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAGTAAACTACTGTTCCAGCACATGCA
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Sequence 27. Application US/10427180

Sequence 27. Application US/10427180

GENERAL INFORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Fincher, Karen

APPLICANT: Wilkinson, Jack

TITLE OF INVENTION: No. 6949696e1 Plant Expression Constructs

FILE REPERENCE: 38.21(51499)B

CURRENT APPLICATION NUMBER: US/10/427,180

CURRENT FILING DATE: 2003-05-01

PRIOR FILING DATE: 2002-05-05

PRIOR PLICATION NUMBER: US/09/737,626

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.0

SEQ ID NO 27

LENGTH 1946
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Best Local Similarity 100.0
Matches 548; Conservative
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GGTGCAGAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCTTTATTGCAAAAGATAAAG 2534
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APPLICANT: Kiehore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Ciesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 409.2; DB 2; 98.1%; Pred. No. 2.1e-80; tive 0; Mismatches 8;
                                                             APPLICALLON.
PILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21(10550)A
TELECOMUNICATION INFORMATION:
TELEPHONE: (314)537-6624
TELEFAX: (314)537-6647
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
TYPE: angle
                         APPLICATION NUMBER: US/08/147,416
                                          FILING DATE: APPLICATION NUMBER: US/07/910,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/07809457A Patent No. 5512466 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.1;
Matches 414; Conservative
        PRIOR APPLICATION DATA:
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Missouri
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US-07-809-457A-17
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APPLICANT: Tumer, Nilgun E.
APPLICANT: Tumer, Nilgun E.
APPLICANT: Julka, Joseph M.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F
STREET: 700 Chesterfield Parkway No. 5503999th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,260
FILING DATE:
CLASSIPICATION: 800
                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                          Score 409.2; DB 2
Pred. No. 2.1e-80;
0; Mismatches 8
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Patent No. 5503999
                                                                            LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-753-738B-6
                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.1%;
Matches 414; Conservative
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFOTENTION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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US-08-368-260-4
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                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F
STREET: 700 Chesterfield Parkway No. 5589612th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,022
FILING DATE:
CLASSIFICATION: 800
                    Virus Resistant Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21(10549) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/910,792
FILING DATE:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
APPLICANT: Jilka, Joseph M.
TITLE OF INVENTION: Virus R
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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Pred. No. 2.1e-80;
0; Mismatches 8; Indels 0
                                                                                                                             SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/809,457A
FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-148-022-5
; Sequence 5, Application US/08148022
; Patent No. 5589612
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
                                                                                                                                                                                                                                                                                                                                        NAME: HOEFIGE Jr., Dennis R. REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-TELECOMMUNICATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 597 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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Best Local Similarity 98.1
Matches 414; Conservative
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    COUNTRY:
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547 AA 548

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2595 CACTCACTAATGCGTATGACGAACGCAGACGACCACAAAAGAATTAGCTTGAGCTCAG 2654
487 CACTCACTAATGCGTATGACGAACGCAGTGACGACCACAAAAGAATTCCCTCTATATAAG 546
                                                                                    2475 GGIGCAGAATIGITAGGCGCACCTACCAAAAGCATCTTIGCCTTTATIGCAAAGATAAAG
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                                                                                                                                         367 GGTGCAGAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCTTTATTGCAAAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08306063
Sequence 1, Application US/08306063
Sequence 1, Application US/08306063
Sequence 1, Sedification:
APPLICANT: Barry, Gerard F.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOSENT INFORMATION:
NAME: HOSENT INFORMATION:
NAME: HOSENT INFORMATION:
REGISTRATION NUMBER: 30,914
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TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
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MOLECULE TYPE: DNA (genomic)
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LENGTH: 597 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                 2655 GA 2656
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                                                                                                  Sequence 1, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF ENVENTION: 5-Enolpyruvylehikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 409.2; DB 2; Length 597;
Pred. No. 2.1e-80;
0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: P. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: MISSOURI
COUNTRY: MISSOURI
ADDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/306,063
PRIOR APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 13-SEP-1997
FILING DATE: 13-SEP-1990
CLASSIFICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-476-008-1
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Best Local Similarity 98.1%;
Matches 414; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                     RESULT 13
US-08-476-008-1
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                                                                    2235 AATTCTCAGTCCAAAGCCTCAACAGGTCAGGGTACAGAGTCTCCAAACCATAGCCAAA
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                         Gaps
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APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 17-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOSTINE JG: DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOSTINE JG: DEC-1990
ATTORNEY/AGENT INFORMATION:
REPERENCE/DOCKET NUMBER: 30.914
REPERENCE/DOCKET NUMBER: 30.914
TELECOMMUNICATION INFORMATION:
Pred. No. 2.1e-80;
0; Mismatches 8;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5702933
GENERAL INFORMATION:
    98.1%;
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Best Local Similarity 98.1
Matches 414; Conservative
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                                                                                                                                                                                                                      Length 597;
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                                                                                                                                                                                                                    Score 409.2; DB 2;
Pred. No. 2.1e-80;
0; Mismatches 8;
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Job time : 952.807 secs
                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.1%;
Matches 414; Conservative
TELEFAX: (314)537-6047 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                 597 base pairs
                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2655 GA 2656
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March 31, 2006, 06:58:31 ; Search time 2211.86 Seconds (without alignments) 10767.297 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2880
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 28, Sequence 28, Sequence 1, A Sequence 27, Sequence 28 Description Sequence Sequence Sequence Sequence Sequence Sequence 1 Sequence Sequence Sequence S Sequence 6 Sequence 6 Sequence 6 Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-737-626A-28 US-10-427-169-28 US-10-909-860-28 US-09-924-197-1 US-09-737-626A-27 US-09-737-626A-27 US-10-927-169-27 US-10-427-180-27 US-10-427-180-27 US-10-909-869-27 US-10-909-869-27 US-10-909-869-27 US-10-970-869-27 US-10-970-869-27 US-10-970-869-27 US-10-970-978-17 US-10-376-763A-17 US-10-376-763A-6 US-09-923-109-6 US-10-164-204-6 US-10-705-430-6 SUMMARIES Length DB 1695 1695 1822 1946 1946 1946 1042 10846 10846 10846 10900 10900 Query 409.2 409.2 409.2 Score 409.2 409.2 409.2 Result No. 

Sequence 13, Appl	Sequence 6, Appli	Sequence 5, Appli	Sequence 29, Appl	Sequence 45, Appl	Sequence 37, Appl	Sequence 38, Appl	Sequence 7, Appli	Sequence 14, Appl	Sequence 12, Appl	Sequence 386, App	Sequence 386, App	Sequence 240, App	Sequence 131, App	Sequence 328, App	Sequence 240, App	Sequence 1922, Ap	Sequence 1, Appli				
US-10-376-763A-13	US-09-522-334-6	US-09-522-334-5	US-10-380-935-29	US-10-012-070A-45	US-10-380-935-37	US-10-380-935-38	US-10-415-305-7	US-10-415-602-14	US-09-737-626A-12	US-10-427-169-12	US-10-427-180-12	US-10-909-860-12	US-10-920-869-12	US-10-473-126-386	US-10-473-126-386	US-10-473-126-240	US-10-240-453-131	US-10-473-126-328	US-10-473-126-240	US-10-311-455-1922	US-10-312-841-1
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## ALIGNMENTS

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LOCATION: (1)..(1695)

OTHER INFORMATION: n=a or g or c or t/u, r=g or a, y=t/u or c

OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intructor. 05-09-737-626A-28
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  Sequence 28, Application US/09737626A

Fatent No. US20020443041

GENERAL INFORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Fincher, Karen

APPLICANT: Fincher, Stanislaw

APPLICANT: Milkinson, Jack

TILE OF INTENTION: No. US20020144304Alel Plant Expression Constructs

FILE REFERENCE: 38-21(1499)

CURRENT APPLICATION NUMBER: US/09/737,626A

CURRENT APPLICATION NUMBER: 09/737,626

FRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0

SEQ ID NO 28

LENGTH: 1695
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121 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
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OCTRION: (1)..(1695)
OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
OTHER INFORMATION: chimeric promoter fusion FWV and EF1 polynucleotides +
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PUblication No. US20030199682A1
GENERAL INFORMATION:
APPLICANT: Flasinski, Stanislaw
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
APPLICATION NUMBER: US/10/427,180
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/09/737,626A
PRIOR APPLICATION NUMBER: 09/737,626
PRIOR PELING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 28
LENGTH: 1695
                                              2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAGACAAAAAAGGAAT
                                                                       301 CAGATTCCTCTAGTACAAGTGGGGAACAAATAACGTGGAAAAGAGCTGTCCTGACAGCC
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US-10-427-180-28
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| Sequence 28, Application US/10427169
| Publication No. US20030199681A1
| GENERAL INFORMATION:
| APPLICANT: Fincher, Karen
| APPLICANT: Fincher, Karen
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: No. US20030199681A1e1 Plant Expression Constructs
| TITLE REFERENCE: 38-21(51499) B
| CURRENT APPLICATION NUMBER: US/10/427,169
| CURRENT FILING DATE: 2003-05-01
| PRIOR PLILING DATE: 2002-02-25
| PRIOR PLILING DATE: 2002-02-25
| PRIOR PLILING DATE: 2000-12-15
| PRIOR PLILING DATE: 2000-12-15
| PRIOR PLILING DATE: 2000-12-15
| PRIOR PLILING DATE: 2001-2-15
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COTHER INFORMATION: \alpha or \alpha or \alpha or \alpha, \alpha = \alpha or \alpha.

OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides US-10-427-169-28
                         GGTGCAGAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCTTTATTGCAAAGATAAAG
                                                     301 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAAGAGCTGTCCTGACAGCC
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100.0%; Pred. No. 3.9e-115;
tive 0; Mismatches 0;
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Matches 646; Conservative
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LOCATION: (1)..(1695) if or c or t/u, r = g or a, y = t/u or c is other information: n= a or g or c or t/u, r = g or a, y = t/u or c is other information: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intructor-920-869-28
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GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Stanislaw
APPLICANT: Milkinson, Jack
ITLE OF INVENTION: ONVel Plant Expression Constructs
FILE REFERENCE: 38-21(51499) B
CURRENT FILING DATE: 2004-08-18
FRIOR FILING DATE: 2004-08-18
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH AND 28
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| OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
| OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intrd
|US-10-909-860-28
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US-10-909-860-28

Sequence 28, Application US/10909860

Sequence 28, Application US/10909860

Publication No. US20050005332Al

GENERAL INFORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Wilkinson, Jack

TITLE OF INVENTION: Novel Plant Expression Constructs

FILE REFERENCE: 39-21 (51499) B

CURRENT FILING DATE: 2004-08-02

PRIOR PELICATION NUMBER: US/10/909,860

CURRENT FILING DATE: 2000-12-15

PRIOR PELICATION NUMBER: 09/737,626

PRIOR FILING DATE: 2000-12-15

PRIOR PELICATION NUMBER: 09/737,626

PRIOR PELICATION NUMBER: 09/737,626
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Best Local Similarity
Matches 559; Conserv
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US-09-737-626A-27
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Publication No. US20030018993A1
GENERAL INFORMATION:
APPLICANT: Gutterson, Neal
APPLICANT: Oeller, Paul
TITLE OF INVENTION: Repeat Sequences
FILE REFERENCE: 012176-010810US
CURRENT APPLICATION NUMBER: US/09/924,197
CURRENT FILING DATE: 2001-08-07
PRIOR FILING DATE: 2000-08-15
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            Length 1695;
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             22.4%; Score 646; DB 8; Le
100.0%; Pred. No. 3.9e-115;
iive 0; Mismatches 0;
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          Query Match
Best Local Similarity 100.0
Matches 646; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 5822
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US-09-924-197-1
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Patent No. US20020144304A1
Patent No. US20020144304A1

RAPPLICANT: Fincher, Karen
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. US20020144304A1el Plant Expression Constructs
FILE REFERENCE: 38-21 (51499) B
CURRENT APPLICATION NUMBER: US/09/737,626A

FILE REPRESSION DATE: 2002-02-25
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
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100.0%; Pred. No. 4.5e-96;
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Best Local Similarity
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Gaps ;

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LOCATION: (1)..(1946)
OTHER INFORMATION: chimeric promoter fusion FMV and Actl1 polynucleotides + Actl1
OTHER INFORMATION: ntro
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APPLICANT: Flasinski, Stanislaw
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: NO. US20030199682A1el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)8
CURRENT PEPLICATION NUMBER: US/10/427,180
CURRENT PEPLICATION NUMBER: US/09/737,626A
PRIOR PILING DATE: 2002-02-25
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Version 3.0
SEQ ID NO 7.7
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    100.0%; Pred. No. 4.5e-96;
                        0; Mismatches
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Best Local Similarity 100.
Matches 548; Conservative
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OTHER INFORMATION: chimeric promoter fusion FMV and Actl1 polynucleotides + Actl1
OTHER INFORMATION: ntro
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Fublication No. US20030199681A1

GENERAL INFORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Fincher, Karen

APPLICANT: Fincher, Karen

APPLICANT: Wilkinson, Jack

TITLE OF INVENTION: No. US20030199681A1e1 Plant Expression Constructs

FILE REFERENCE: 38-21(51499)B

CURRENT APPLICATION NUMBER: US/10/427,169

CURRENT PILING DATE: 2003-05-01

PRIOR APPLICATION NUMBER: US/09/737,626

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.0

SEQ ID NO 27

LENGTH: 1946
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                                             AATTCTCAGTCCAAAGCCTCAACAAGGTCAGGGTACAGAGTCTCCAAACCATTAGCCAAA
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  Matches 548; Conservative
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NAME/KEY: promoter
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19.0%; Score 548; DB 6; Length 1946;

Query Match

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NAME/KEY: promoter
LOCATION: (1). (1946)
OTHER INFORMATION: chimeric promoter fusion FMV and Actl1 polynucleotides + Actl1
OTHER INFORMATION: ntro
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Publication No. US20050022261A1

GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Flasinski, Stanislaw
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
ITLE OF INVENTION: UNOVEL Plant Expression Constructs
ITLE OF INVENTION: WUMBER: US/10/920,869
CURRENT FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
PRIOR PLING DATE: 2000-12-15
PRIOR PLING DATE: 2000-12-15
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: US/09/737,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: US/09/737,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 109/137,626
PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR PRIOR PLING DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR PRIOR PRIOR PRIOR DATE: 2000-12-15
SRIGH APPLICATION NUMBER: 105/09/737,626
PRIOR P
                              Score 548; DB 8; 1
Pred. No. 4.5e-96;
             ORGANISM: artificial sequence
                              Query Match
Best Local Similarity 100.0
Matches 548; Conservative
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FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1946)
OTHER INFORMATION: chimeric promoter fusion FMV and Actl1 polynucleotides +
OTHER INFORMATION: ntro
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19.0%; Score 548; DB 6; Length 1946;
                                                             Indels
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| Publication No. US2005005332A1
| GENERAL INFORMATION:
| APPLICANT: Flasinski, Stanislaw
| APPLICANT: Flasinski, Stanislaw
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: Novel Plant Expression Constructs
| TITLE OF INVENTION NUMBER: US/10/909, 860
| CURRENT FILING DATE: 2004-08-02
| PRIOR APPLICATION NUMBER: US/09/737,626
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0
                              100.0%; Pred. No. 4.5e-96; ive 0; Mismatches 0;
                           Best Local Similarity 100.
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APPLICANT: Barry, Gerard F.
APPLICANT: Barry, Gerard F.
APPLICANT: Balore, Ganesh M.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899-10175. CUNSOI MOBT: 175-2
CURRENT PELLORION NUMBER: US/09/464,099A
CURRENT PELLING DATE: 1999-12-16
FRIOR FILING DATE: 1999-08-20
FRIOR FILING DATE: 1997-04-07
FRIOR FILING DATE: 1997-04-07
FRIOR FILING DATE: 1997-04-07
FRIOR FILING DATE: 1991-08-28
FRIOR FILING DATE: 1991-08-28
FRIOR FILING DATE: 1990-08-31
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                                                                                                                                       Length 597;
                                                                                                                                       Score 409.2; DB 3; Length
Pred. No. 2.5e-69;
0; Mismatches 8; Indels
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; Patent No. US20020168680A1
; GENERAL INFORMATION:
                             ; TYPE: DNA
; ORGANISM: Figwort mosaic virus
US-09-861-696-1
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                                                                                                                                          Query Match
Best Local Similarity 98.1%;
Matches 414; Conservative
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     LENGTH: 597
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j Sequence 1, Application US/09861696

j Patent No. US20020007053A1

j GENERAL INFORMATION:

APPLICANT: Rishore, Ganesh M.

APPLICANT: Radgette, Stephen R.

APPLICANT: Padgette, Stephen R.

APPLICANT: Padgette, Stephen R.

APPLICANT: Padgette, Stephen R.

APPLICANT: Stallings, William C.

APPLICANT: Padgette, Stephen R.

APPLICANT: Stallings, William C.

APPLICANT: Stallings, William C.

CURRENT APPLICATION NUMBER: US/09/861,696

CURRENT APPLICATION NUMBER: US 09/137,440

PRIOR APPLICATION NUMBER: US 08/33,485

PRIOR PILING DATE: 1994-09-13

PRIOR PILING DATE: 1994-09-13

PRIOR PILING DATE: 1994-09-13

PRIOR PILING DATE: 1994-09-13

PRIOR PILING DATE: 1990-08-28

PRIOR PILING DATE: 1990-08-28

PRIOR PILING DATE: 1990-08-31

PRIOR PILING DATE: 1990-08-31

SOPTWARE: PatentIn version 3.0

SEQ ID NO 1
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                                                        Score 548; DB 8; Length 1946;
Pred. No. 4.5e-96;
                                                                                                          0; Indels
                                Query Match
Best Local Similarity 100.0
Matches 548; Conservative
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US-10-920-869-27
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                                              753 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAAGAGCTGTCCTGACAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: expression OTHER INFORMATION: cassette comprising plant operable promoter linked OTHER INFORMATION: to a coding sequence encoding an AMPA OTHER INFORMATION: acetyltransferase linked to a transcription OTHER INFORMATION: termination sequence
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Publication No. US20030106096A1
GENERAL INPORMATION:
FIGE REPRINCE: 38-24 [15.503)
FILE REFERENCE: 38-24 [15.503)
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT APPLICATION NUMBER: US/09/441,340
FRIOR FILING DATE: 1999-11-16
FRIOR APPLICATION NUMBER: 05/108,763
FRIOR FILING DATE: 1999-11-17
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: PATCHING DATE: 1998-11-17
SEQ ID NOS: 32
SEQ ID NOS: 32
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Pred. No. 3.8e-69;
0; Mismatches 8;
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Best Local Similarity 98.1%;
Matches 414; Conservative 0
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ORGANISM: Artificial Sequence
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; LOCATION: (1350)..(1605)
US-10-213-791-23
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LOCATION: (893)..(1324)
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NAME/KEY: promoter
LOCATION: (33)..(60
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US-10-213-791-23
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        Length 597;
                                          Indels
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Publication No. US20040172669A1
GERERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION UNMBER: US/10/376,763A
CURRENT APPLICATION DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
    Score 409.2; DB 3;
Pred. No. 2.5e-69;
0; Mismatches 8;
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OTHER INFORMATION: PCR product
      14.2%;
98.1%;
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Query Match
Best Local Similarity 98.1
Matches 414; Conservative
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US-10-376-763A-17
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Biocceleration Ltd.
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Copyright (c) 1993 - 2006
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Listing first 45 summaries
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Add95182 pWON75571
Aeb71496 A. tumefa
Add71896 A. tumefa
Add1556 pWON33828
Add15562 pWON33828
Add15562 pWON33829
Add1562 pWON33829
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Adv69212 Vector pC
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ADO95182 AEB71496 ADO95181 AAA15563 AAA15564 AAA15564 AAA155627 ABL54627 ADV39082 AVY39062 AVY39062 AVX30622 AANS0226 ABANS0226 ABANS0226

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2005s:\*

geneseqn2003cs:\*

SUMMARIES

## AAX5730 Sugar bee AAX5730 Sugar bee AAX5730 Sugar bee AAX68923 Wecror co AAX08924 Wecror co ABS54337 B. coll f Adg1358 Plasmid p Adw69411 EIF-5A wo Abv76269 Expressio Abv75876 Luciferas Abv75875 Luciferas AAC66931 Plant sig AAC66931 Plant sig Adr46166 Glyphosat Adr49368 H7-1 tran Adr49367 Vector pV Aeb71496 A. tumefa ADR49368 ADR49367 ABB71496 AAX57309 AAX57309 AAX57309 AAX57308 AAX6923 AAX08924 ABX08924 ABX08924 ABX08924 ABY08924 ABY089811 ABY089811 ABY76876 ABV76876 AAC66931 ABN83922 ADU73233 BB Length 3778 7794 8012 8418 8798 10846 10900 10900 662 1998 12304 12497 12614 632 5365 Query Match 1 Result No. U

Claim 5; SEQ ID NO 4; 50pp; English.

XX PS

Adu73233 Plasmid

REST ADR4	KESULT 1 ADR46166
	ADR46166 standard; DNA; 1675 BP.
×	
S. A.	ADR46166;
į	10-MAY-2004 (finat cateur)
ξŽ	
X	Glyphosate resistance cotton event MON 88913 3' DNA junction sequence.
₹	Glyphosate tolerance; herbicide tolerance; cotton; transgenic; plant;
X X	MON 88913; gene; ds.
88	Gossvoium hirsutum.
SO	Agrobacterium sp.
SO	Chimeric.
į	Touristical/Analitations
G E	di fforondo
: 5	/*+30
: E	=
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NA S	WO2004072235-A2.
<b>\$</b> 6	26 - bitc - 2004
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PF	02-FEB-2004; 2004WO-US002907.
×	
짪	12-FEB-2003; 2003US-0447184P.
X:	
Z Z	(MONS ) MONSANTO TECHNOLOGY LLC.
Id	Cerny RE, Duong C, Hart JL, Huber SA, Krieb RL, Listello JJ;
PI	B, Sammons B;
×	
DR	WPI; 2004-625846/60.
×	
ᅜ	event designated MON 88913, useful for produc
ΡŢ	cotton plant that tolerates application of glyphosate herbicide to
H	control weeds in crop.

The present sequence is the 3' transgene/genomic junction sequence of glyphosate tolerant cotton event MON 88913. This sequence is novel in cotton event MON 88913. A cotton plant and seed comprising the Sequence in its genome is an aspect of the invention. Cotton event MON 88913 was generated by an Agrobacterium-mediated transformation of cotton cells continued by an Agrobacterium-mediated transformation of cotton cells cransgene expression caseettes that each included a glyphosate tolerant 5 corton event MON 88913 having seed deposited at ATCC PTA-4854, and to progeny plants and seeds or their regenerable parts, and cotton plants are also provided for detecting the presence of DNA corresponding to cotton event MON 88913 in cample by detecting a transgency genomic junction region from cotton cample by detecting a transgency genomic junction region from cotton cused in a DNA amplification method to produce an amplicon comprising the cused in a DNA amplification method to produce an amplicon comprising the provided are methods of producing glyphosate tolerant MON 88913 in cused in a DNA amplification method to produce an amplicon comprising the provided are methods of producing glyphosate tolerant cotton plants, and amethod for determining the zygosity of the progeny of cotton event MON 89913. Also provided are methods of producing glyphosate tolerant cotton plants, and amethod for determining the zygosity of the progeny of cotton event MON 89913. Also provided are methods of producing glyphosate tolerant cotton plants, and amethod for determining the zygosity of the progeny of cotton event MON 89913. Also provided are methods of producing glyphosate tolerant cotton plants, and amethod for determining the zygosity of the progeny of cotton event MON 89913. Also provided are methods of producing glyphosate tolerant cotton plants, and amethod for determining the zygosity of the progeny of cotton event MON 89913. Also provided are methods of producing glyphosate tolerant cotton event MON 89913. Also provided are meth event MON 88913 by applying glyphosate herbicide. ×66666666666666666666666666666666666

Sequence 1675 BP; 633 A; 221 C; 190 G; 631 T; 0 U; 0 Other;

	<b>'</b> 0		09	120	120	180	180	240	240	300	300	360	360	420	420	480	480	540	540	009	009	099	660
100.0%: Score 167	nilarity 100.0%; Pred. No. 1.5e-185; Conservative 0; Mismatches 0; I	1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA	. TGACCGAAGTTAATATGAGGAGTAAAACACTTGTGTGTGT	GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGT	GGCAACAAATATATTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC	. CTCTTGTGTTTTAGACATTTATGAACTTTCCTTATGTAATTTTCCAGAATCCTTGTCAG	. CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG	ATTCTAATCATTGCTTTATAATTATAGGTTATACTCATGGATTTGTAGTTGGGTATGAAAA	. ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA	TATITITAATGCATTTTATGACTTGCCAATTGATTGACAACAAGCATCAATCGACCTGC	. TATTTTTAATGCATTTTATGACTTGCAATTGACATGCATG	AGCCACTCGAGTGGAGGCCTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGA		AATAAAGATTTCCGAATTAGAATAATTTGTTTATTGCTTTCGCCTATAAATACGACGGAT	. AATAAAGATTTCCGAATTAGAATAATTTGTTTTTTTTCCTTTCGCCTATAAATACGACGGAT	CGTAATTTGTCGTTTTATCAAAATGTACTTTCATTTTATAATAACGCTGCGGACATCTAC	. CGTAATTTGTCGTTTTATCAAAATGTACTTTCATTTTATAATAACGCTGCGGACATCTAC	ATTITIGAATIGAAAAAAAATIGGTAATITACTCTITCTTTTTTCTCCATATIGACCATCAT	ATTTTGAATTGAAAAAAATTGGTAATTACTCT	ACTCATTGCTGATCCATGTAGATTTCCCGGACATGAAGCCATTTACAATTGAATATATAT	. ACTCATTGCTGATCCATGTAGATTTCCCGGACATGAAGCCATTTACAATTGAATATATAT	TACAAAGCTATTTGCTTATAACATATGCGAAAAATTTTGTACTATAATCAGGGGTAAATT	TACAAAGCTATTTGCTTATAACATATGCGAAAATTTTGTACTATTATGAAATTT
Ouerv Match	Best Local Sig Matches 1675;	-	H	61	61	121	121	181	181	241	241	301	301	361	361	421	421	481	481	541	541	601	100
One	Best Match	ò	QQ	δ	d Q	ò	qq	ò	qq	ò	d G	ò	ą	ò	e G	ò	qq	ò	ф	ò	d Q	ò	1

661	TAGGAGGGGCTTGTAGGTCTCGCTTCTTAAAATGAAAAATTTTCTATTTAGTTATTT 720 
AAA.	TITITAAAAGTAAAATTATAAAATTTCATTTAATCCTTTAAAAATTATAAAGATATA 780
GA C	NITITAHANGIAHANATATATAANATITATATITATAANATTATAATITATAATITATAATATTGGAC 840
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0 0 0 0 0	TAACAAAATTTTCTGATTTTGCCCCTAACTGTAATATTTGTATAAAACATTTTCTT 900
TTT	GCATTTAATGATTTCTTTAATTCGAGGAAGAAGAAATTTATTAATTGCATATGCG 960
-LL	GCATITAATGATITCTTTAATTCAGICCAAGAAAGAAATTTATTAATTGCATAIGCG 960
<b>*</b> =	GTTAGTCCTTGCCTAGTGATATTAAAGGAAAGAAACATAAAATCAATAAATTTT 1020
¥ i	GTTAGTCCTTGCCTAGTGATATTTAAAGGAAACATAAATTAATT
	AAGCAANTAGTAAAAATTAAGSAAAAACTITCTAGGATAGTCTATAATTCAAAAAAAG 1080 
<b>X</b> =	TAATAATCTTTAACCATTGAATTTTAAAATAACATCAGAATAATCTATTTATT
-A	TAATAATCTTTAACCATTGAATTTTAAAATAACATCAGAATAATCTATTTATT
t=t	atrartratracentratritratratratrara   1200 
AAT	CAATAAAAATTTCTTACAAAATAAATTATATTTTGAGGGTGTTTTATTATTTT 1260
AAT	CAATAAAAATTTCTTACAAATAAATTATATTTTTGAGGGTGTTTTATTTTT 1260
ATA	TATTTTATACAGACATATAGAAATATAAATACACATAATAAAAATTTGAATCCAAATT 1320
ATA	TATTTTATACAGACATATAGAAATATAAATACACATAATAAAATTTGAATCCAAATT 1320
	321 TTTAATTTTTAACATTTATAATTTACTATTCAACCAAAATTTTATTTATTTATTTATTA
381 AAT	TTTTATAAATATATTTATCAGATAATGCGATTTTTTTACCTATATATA
AAT	TTTTATAAATATATTTTATCAGATAATGCGATTTTTTTACCTATATATA
AAT	CTACTITAAATTAAGTCCTAAAAATAATATATCATACCAAAAAAATTCTTAAAATGA 1500
AAT	CTACTITAAATTAAGTCCTAAAAATAATATATCATACCAAAAAAATTCTTAAAATGA 1500
ATC	TGATAATACTTAACCCCTTTATAAAACAATCTTAACCCCTTATATATTTTAATATT 1560
	>>>
<b>A</b> = <b>a</b>	ATCATTATAAATATAAATCTATTGAGCATATGTTTTAAACCAAGTAATGTTGAGTGC
GG	AGTAAAACTCATTACACATTTTAAGTAGAACGTAGTTCGAACCTTGGAGAAG 1675

RESULT 2 ADR49368 ID ADR49368 standard; DNA; 3706 BP.

ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGAAA 3271

ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA

CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 180

CTCTTGTGTTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG

TATITITIAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC 300

AGCCACTCGAGTGG------

AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA

TITGITITATIGCTITICGCCTATAAATACGACGGATCGTAATITIGTCGTTTTTATCAAAAIG

TACTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTTGAATTGGT

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--- AGGCCTCATCT

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CTITITICTCCATATIGACCATCATACTCATTGCTGATCCATGTAGATTT

CCCGGACATGAAGCCATTTACAATTGAATATATATA 602

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3512 TACTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTGAATTG-AAAAAATTGGT 3570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3571 AATTACTCTTTCTTTTTCTCCATATTGACCATACTCATTGCTGATCCATGTAGATTT 3630
                                                                                                                                                                                                                                                                           3392 AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA 3451
                                                                                                                                                                                                                                                                                                                                                    3452 TTTGTTTATTGCTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTATCAAAATG 3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3631 CCCGGACATGAAGCCATTTACAATTGAATATATCCTA 3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR49367 standard; DNA; 3778 BP
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ADR49367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel glyphosate-resistant Glycine max (sugar beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The invention also describes a method for identifying glyphosate-tolerant beet, cugar beet and a test kit for identifying glyphosate-tolerant sugar beet, or their cells, tissues and parts. The novel kit comprises at least one primer recognizes a foreign DNA inserted into the genome, while the second recognises DNA within a flanking (3' or 5') region. The plants are prepared by Agrobacterium-mediated transformation of sugar beet, using the vector pV-BVGT08, which contains, between right and left border sequences, a cassette containing the coding regions for (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl-shikimate-3-phosphate synthase (BPSPS) from Arabidopsis thaliana, under control of the figwort mosaic virus promoter and the BD-3' control of the figwort mosaic virus promoter and the BD-3' transformation event (H7 control of the figwort mosaic virus promoter and the BD-3' transcriptional terminator of Pisum sativum. One transformation event (H7 control of the fluorit to contain an insertion of a single, intext copy of the T-DNA, including the regulatory components, from pV-BVGT08. The genomic sequences outside the insert region were identical with those in a non-transformed plant and the insert was integrate stably and inherited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  properties as regards growth, yield, quality and resistance to ogens. This sequence represents a fragment of the H7-1 transformant
                                                                                                                           glyphosate-tolerant sugar beet; chloroplast transit peptide;
5-enolpyruvyl-shikimate-3-phosphate synthase; BPSPS; H7-1 transformant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stably. The novel plants are highly resistant to glyphosate and retain
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New sugar beet plants resistant to glyphosate, contain inserted enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 530.6; DB 13; Length 3706; 92.9%; Pred. No. 2.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3706 BP; 943 A; 801 C; 801 G; 1161 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  Loock A, Jansen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.8e-53;
                                                                           H7-1 transformant-associated DNA fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 6; 79pp; German.
                                                                                                           plant; glyphosate-resistance;
                                                                                                                                                                                                                                                                                                                                                                                                  Nehls R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNA found in vector pV-BVGT08
                                                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003EP-00003866.
28-FEB-2003; 2003US-00376763.
                                                                                                                                                                                                                                                                                   17-FEB-2004; 2004WO-EP001469
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated and inherited.
                                                                                                                                                                                                                                                                                                                                                                                                  Sauerbrey E,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-652964/63.
                                                                                                                                                                                                                                                                                                                                                                    (KWSS-) KWS SAAT AG.
                                                                                                                                                         T-DNA; CP4-EPSPS.
                                                                                                                                                                                                                      WO2004074492-A1
                                                                                                                                                                                        Unidentified
                                            18-NOV-2004
                                                                                                                                                                                                                                                      02-SEP-2004
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                ADR49368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ds; plant; glyphosate-resistance; sugar beet; seed; glyphosate-tolerant sugar beet; chloroplast transit peptide; 5-enolpyruvyl-shikimate-3-phosphate synthase; BPSPS; H7-1 transformant; T-DNA; pV-BVGTO8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New sugar beet plants resistant to glyphosate, contain inserted enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably integrated and inherited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loock A,
                                                     Vector pV-BVGT08 H7-1 transformant insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nehls R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2003; 2003EP-0000386.
28-FEB-2003; 2003US-00376763.
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(first entry)
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                                                                                                                                                                                                                                                                                                WO2004074492-A1.
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                                                                                                                                                                                                                                             Synthetic
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TGACCGAAGTTAATATGAGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 3091

3032

8 유 8 셤

TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA

9

36; Gaps

9; Indels

0; Mismatches

Best Local Similarity .... Matches 592; Conservative

3092 GGCAACAATTATTTTCAGACCTAGAAAGCTGCAAATGTTACTGAATACAAGTATGTC 3151 GGCAACAAATATATTTTCAGACCTAGAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120

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CDS
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                                             유
                                                        This invention describes novel glyphosate-resistant Glycine max (sugar beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The invention also describes a method for identifying glyphosate-tolerant sugar beet, or their cells, tissues and parts. The novel kit comprises at least one primer pair, where one primer recognizes a foreign DNA inserted into the genome, while the second recognises DNA within a flanking (3' or 5') region. The plants are prepared by Agrobacteriuu-mediated transformation of sugar beet, using the vector pV-BVGT08, which contains, between right and left border sequences, a cassette containing the coding regions for (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl.

CC (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl.

CC shikimate-3-phosphate synthase (EPSPS) from Arabidopsis thaliana, under control of the figwort mosal or virus promocer and the EB-3'

CC characterised and found to contain an insertion of a single, inteact copy of transcriptional terminator of pisum sativum. One transformation event (H7 of the T-DNA, including the regulatory components, from pV-BVGT08. The genomic sequences outside the insert region were identical with those in casellably. The novel plants are highly resistant to glyphosate and retain cool pathogenes. This sequence represents the vector pV-GVGT08 H7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3077 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 3136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3137 GGCAACAAATATATTTTCAGACCTAGAAAGCTGCAAATGTTACTGAATACAAGTATGTC 3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3317 TATTITIAATGCATTITATGACTTGCCAAFTGATTGACAACATGCATGCATCAATGGCCTGC 3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3616 AATTACTCTTTCTTTTTCTCCCATATTGACCATCATACTCATTGCTGATCCATGTAGATTT 3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 TTTGTTTATTGCTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTATCAAAATG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1557 TACTITICATITITATAATAACGCIGCGGACAICCTACATITITIGAATIG-AAAAAATIGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.7%; Score 530.6; DB 13; Length 3778; Best Local Similarity 92.9%; Pred. No. 2.8e-53; Matches 592; Conservative 0; Mismatches 9; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3778 BP; 958 A; 822 C; 823 G; 1175 T; 0 U; 0 Other;
SEQ ID NO 5; 79pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AGCCACTCGAGTGG
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   Claim 14;
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566 CCCGGACATGAAGCCATTTACAATTGAATATATTA 602

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product= "A. tumefaciens EPSPS chloroplast transit
                                                                                                                                                                                                                                                                                                                                                                                                           note= "Zea mays alpha zein gene Z22asL fragment
                                                                                                                                                                                                                                                                                                                                                   *tag= g
'note= "Zea mays alpha zein gene Z19s fragment"
                                                                                                                                                                                                                                                                                                                                                                                   note= "Zea mays alpha zein gene Z22s fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Zea mays gamma zein gene Z27 promoter"
353. .7794
                                                                                                                                                                                                                                                                                                                                 note= "Pisum satiuvum RbcS2 terminator"
                                                                                                                                                                                                              '*tag= b
'note= "Rice actin promoter and intron"
                                                                                                                                                                                                                                                                                                          tumefaciens NOS terminator"
                                                                                                     SEQ ID NO:2.
                                                                                                                                                                                              tumefaciens right border"
3676 CCCGGACATGAAGCCATTTACAATTGAATATATCCTA 3712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= 1
/note= "A. tumefaciens left border"
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                                                                                                                                                                                                                                                                                 "A. tumefaciens aroA"
                                                                                                                      vector; recombinant DNA; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     zein
                                                                                                    A. tumefaciens transformation vector DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Zea mays alpha
7204. 7305
                                                                                                                                                                      Location/Qualifiers
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                                                  AEB71496 standard; DNA; 7794
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                                                                                                                                                                                                                                                               20<u>1</u>2. .3379
/*tag= d
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/*tag= a
/note= "A.
376. .1774
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3479. .4391
                                                                                    (first entry)
                                                                                                                                     Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                 product=
                                                                                                                                                                                                                                                        eptide"
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(MALV/) MALVAR T |
(LUET/) LUETHY M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005176670-A1
                                                                                                                                              Pisum sativum
                                                                                                                                                                      Key
misc_feature
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                                                                                    20-0CT-2005
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                                                                    AEB71496;
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                                   RESULT 4
AEB71496/c
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AAX57309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel recombinant DNA construct for suppression of at least one target gene. The recombinant DNA construct comprises in 5' to 3' order a promoter element operably linked to an antisense-oriented DNA element from at least one target gene and a sense-oriented DNA element, where the sense oriented DNA element is shorter than the anti-sense oriented DNA element, and sense oriented DNA element is shorter transcribed by the sense oriented DNA element, and sense oriented RNA transcribed by the anti-sense oriented DNA element, wherein the transcribed RNA forms a into a loop of anti-sense oriented DNA element, wherein the transcribed RNA forms a into a loop of anti-sense oriented RNA forms a linto a loop of anti-sense oriented RNA forms a linto a loop of anti-sense oriented RNA forms a linto a loop of anti-sense oriented RNA forms a linto a loop of anti-sense oriented RNA for suppressing the at least one target gene. Also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4040 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 3981
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                                                                 element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                        is a method for generating anti-sense oriented RNA in an organism for suppression of a target gene, comprising providing in cells of the organism a recombinant DNA construct which is transcribed to RNA that forms a loop of anti-sense oriented RNA. The methods and compositions of the present invention are useful for producing gene-suppressing loops of anti-sense RNA, and making and using constructs and transgenic plants expressing gene-suppressing loops of antisense RNA and with enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a recombinant DNA construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3980 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTGTGTTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                              New recombinant DNA construct having in 5' to 3' order a promoter operably linked to an anti-sense oriented DNA element, useful for producing transgenic plants expressing gene-suppressing loops of antisense RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 312.8; DB 14; Length 7794; Pred. No. 3.7e-28; 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7794 BP; 2016 A; 1940 C; 1771 G; 2067 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar beet T-DNA containing cp4/epsps fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCACTCGAGTGGAGGCCTCATCTAAGCCCC 332
                                                                                                                                         Example 2; SEQ ID NO 2; 19pp; English.
 Luethy MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%;
96.4%;
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 Malvar TM,
                               WPI; 2005-541778/55
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26-JUL-1999
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 Huang S,
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Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 U; 0 Other;
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Pred. No. 7.8e-28;
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100.0%; Pred. No. ...
0; Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
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Best Local Similarity
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                                                                                                          Beta vulgaris.
                                                                                                                                                                                                                                                                     29-OCT-1998;
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                                                                                                                                                                                                               14-MAY-1999.
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Matches 310;
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2977 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA 3036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2797 IGACCGAAGITAATATGAGGAGTAAAACACTIGIAGITGTACCATTATGCITATICACTA
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                                                                                                                                                                                    Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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                                                                                                                                               Sugar beet T-DNA containing cp4/epsps.
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  BP.
  AAX57308 standard; DNA; 8798
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26-JUL-1999
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Matches
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                                                                                                 Sugar beet, transformation, T-DNA, insertion, cp4/epsps, plant, 5-enolpyruvylshikimate-3-phosphate synthase, transgenic, herbicide, tolerant, glyphosate, Roundup, N-phosphonomethyl-glycine, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                        VERW GES MBH
                                                            Sugar beet T-DNA containing cp4/epsps #2
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Best Local Similarity 100.
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RESULT 7

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TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA

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The present invention relates to a recombinant, double-stranded DNA vector, comprising a promoter functional in plant cells, and a DNA sequence from a prokaryotic organism (e.g. Escherichia coli) coding for fructose-1,6-bisphosphate aldolase (FDA), where the DNA sequence is operatively linked to the promoter in the sense orientation. FDA catalyses the conversion of triosephosphate into fructose-1,6 bisphosphate in plant chloroplasts (starch synthesis) and in the cytosol sucrose synthesis). The recombinant DNA vector of the invention is useful for producing genetically transformed plants that have elevated carbon assimilation, storage, export and improved uniformity of solids (e.g. in transgenic potatoes expressing fda). The vector of the invention is particularly useful in the commercial production of foods derived from potatoes which are useful for producing French fries. The transgenic plants exhibit increased photosynthesis rate, increased plant yield, increased prowth rate and increased solids uniformity compared with plants that do not contain the recombinant DNA vector. The recombinant DNA vector provides higher quality, more uniform potator regions, and therefore french fries. This results in a higher throughput in the French fry processing plant due to lower processing times, and processor cost savings due to lower processing times, and processor cost savings due to lower processing times, and processor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y input required for lower blanch, dry, sequence represents a plant transformation
                                                                                                                                                                                                          Fructose-1,6-bisphosphate aldolase; FDA; triosephosphate; plant chloroplast; starch synthesis; cytosol; sucrose synthesis; carbon assimilation; carbon carbon export; transgenic; potato; food production; French fry; photosynthesis; plant yield; plant growth; potato tuber; blanch; dry; par-fry; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant, DNA molecule for producing genetically transformed plants having elevated carbon assimilation, has promoter functional ir plant cells, and DNA sequence encoding fructose-1,6-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10846 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 0 Other;
                                                                                                                                                                      coli fda gene, plant transformation vector pMON17524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector containing the E. coli fda gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Col 35-44; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barry GF, Cheikh N, Kishore GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MONS ) MONSANTO TECHNOLOGY LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present
                                          ABS54336 standard; DNA; 10846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0049995P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00098219
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis sp.
Figwort mosaic virus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-711539/77.
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                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                            12-DEC-2002
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RESULT 8
                    ABS54336
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                                                                                                                                                                                                                                                                   Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible reaction converting triosephosphate into fructose-1,6-bisphosphate aldolase. By inserting triosephosphate into fructose-1,6-bisphosphate these vectors and inserting the FDA gene into expression vectors and inserting the FDA gene into expression of the FDA enzyme production can be achieved. Increasing the expression of the FDA enzyme in the chloroplast increases carbon assimilation and results in an increase in chloroplast starch production. This increase in carbon assimilation is a desirable trait in crop plants and leads to increased plant growth, storage ability, yield, vigour, and stress tolerance. Increasing FDA expression in the cytosol of photosynthetic cells leads to an increase in sucrose production. The transgenic plants containing the recombinant DNA can have increased photosynthesis rates, increased
                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch; sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;
                                                                                                                                                                                                   ATTCTAATCATTGCTTTATAATTATAGTTATACTCCATGGATTTGTAGTTGGGTATGAAAA
                                                               GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                   CICTIGEGITITIAGACATITATGAACTITICCTITATGTAATTITICCAGAATCCTIGETCAG
TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACTACCATTATGCTTATTCACTA
                                              GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                              CICITGIGITITIAGACATITATGAACTITICCITTATGTAATTTTCCAGAATCCTTGTCAG
                                                                                                                                                                               ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA
                                                                                                                                                                                                                                                 TATTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector comprising fructose-1,6-bisphosphate aldolase (FDA) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 51-54; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX08923 standard; DNA; 10847 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0049955P.
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                                                                                                                                                                                                                                                                                                                                      301 AGCCACTCGA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-095343/08.
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Gaps

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18.5%; Score 310; DB 6; Length 10846; 100.0%; Pred. No. 7.4e-28; Artive 0; Mismatches 0; Indels 0;

Query Match 18.5% Best Local Similarity 100.0 Matches 310; Conservative

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yields, increased growth rates and improved solids uniformity compared with plants that do not contain the recombinant DNA molecule. Vectors containing the recombinant FDA gene are used particularly for improving potato products. This sequence describes the vector designated pMON17524 which comprises the E.coli FDA gene fused to the Arabidopsis small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of fructose-1,6-triphosphate aldolase DNA - useful for, e.g. producing transgenic plants with increased photosynthesis rates, increased growth rates and improved solids uniformity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch; sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;
                                                                                                                                                                                                                                    TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                         GGCAACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                                                                                                                                                                              CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2299 TAITTITTATGCATTTTATGACTTGCCAATTGATTGACAACAAGCATCAATGGACCTGC
                                                                                                                                                                                                                1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                              181 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC
                                                                                subunit CTP1. This vector was used for tobacco plant transformation
                                                                                                                  Sequence 10847 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising fructose-1,6-bisphosphate aldolase (FDA) gene.
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                                                                                                                                              Length 10847;
                                                                                                                                                                              Indels
                                                                                                                                             18.5%; Score 310; DB 2; I 100.0%; Pred. No. 7.4e-28; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 55-58; 75pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US012447.
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCACTCGA 2368
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                                                                                                                                                               Best Local Similarity
Matches 310; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1998;
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Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible reaction converting triosephosphate into fructose-1,6-bisphosphate aldolase. Is aldolase. By inserting the FDA gene into expression vectors and inserting these vectors into the chloroplasts of plant cells, increased starch chase vectors into the chloroplast increases carbon assimilation and results in an increase in chloroplast starch production. This increase in carbon assimilation is a desirable trait in crop plants and leads to increased in chloroplast starch production. This increase in carbon assimilation is a desirable trait in crop plants and leads to increased in sucrose production. The transgenic plants containing the an increase in sucrose production. The transgenic plants containing the crombinant DNA can have increased photosynthesis rates, increased containing the recombinant DNA molecule. Vectors containing the recombinant FDA gene are used particularly for improving pertato products. This sequence describes the vector designated pWON17542 which comprises the E.coli FDA gene fused to the Arabidopsis small subunit CTP1 and the Arabidopsis EPSPS (CTP2) transit peptide. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2179 CTCTTGTGTTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 2238
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10900 BP; 2691 A; 2750 C; 2694 G; 2764 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5%; Score 310; DB 2; Length 10900; 100.0%; Pred. No. 7.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli fda gene, plant transformation vector pMON17542.
                                                                                                                                                                                                                                                                                                                                                                                    vector was used for tobacco plant transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. nc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 310; Conservative
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Arabidopsis sp.
Figwort mosaic virus.
Synthetic.
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ADQ13598 standard; DNA; 11606 BP

(first entry)

23-SEP-2004

ADQ13598;

US6441277-B1

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RESULT 12
ADQ13598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice present interaction teraces to a recombinant cells, and a DNA sequence from a prokaryotic organism (e.g. Escherichia coli) coding for fructoseel, 6-bisphosphate aldolase (PDA), where the DNA sequence is operatively linked to the promoter in the sense orientation. FDA catalyses the conversion of triosephosphate into fructose-1,6 catalyses the conversion of triosephosphate in plant chlorophates (starch synthesis) and in the cytosol (sucrose synthesis). The recombinant DNA vector of the invention is useful for producing genetically transformed plants that have elevated carbon assimilation, storage, export and improved uniformity of solids (e.g. in transgenic potatose expressing fda). The vector of the invention is particularly useful in the commercial production of foods derived from 1 potatos which are useful for producing French fries. The transgenic plants exhibit increased photosynthesis rate, increased plant yield, increased growth rate and increased solids uniformity compared with the recombinant DNA vector. The recombinant DNA vector provides higher quality, more uniform potato tuber regions, and therefore french fries. This results in a higher throughput in the Erench fries this results in a higher throughput in the creates any processing plant due to lower processing times, and processor cost savings due to lower energy input required for lower blanch, dry, and par-fry times. The present sequence represents a plant transformation cortaining the E. coli fda gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2119 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2059 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2239 ATTCTAATCATIGCTTTATAATTATAGTTATACTCAIGGATTIGIAGTAGTAGTAGAAAA 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CTCTTGTGTTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTTCCAGAATCCTTGTCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCAACAATTATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATITITIAATGCATTITATGACTIGCCAATTGATTGACAACATGCATCAATCGACCTGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinant, DNA molecule for producing genetically transformed plants having elevated carbon assimilation, has promoter functional in plant cells, and DNA sequence encoding fructose-1,6-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2179 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a recombinant, double-stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10900 BP; 2691 A; 2749 C; 2695 G; 2765 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Col 45-54; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         Barry GF, Cheikh N, Kishore GM;
                                                                                                                                                                                                                                                                                        (MONS ) MONSANTO TECHNOLOGY LLC.
                                                                                                                                                                                            97US-0049995P.
                                                                                                98US-00098219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-711539/77.
                                                                                                                                                                                       17-JUN-1997;
                                                                                           16-JUN-1998;
27-AUG-2002
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The invention relates to a new polynucleotide comprising (i) a nucleotide sequence encoding a mutant plant ethylene receptor protein, or its sequence encoding a mutant plant ethylene receptor protein, or its cargament, which exhibits ethylene insensitivity, and (ii) a regulatory nucleotide sequence promotes transcription mucleotide sequence promotes transcription of the protein encoding nucleotide sequence in cells that comprises abscission zone tissue of a plant. Also included are a cell transformed with the polynucleotide, a plant, plant tissue, or a plant cell transformed with nor bred to contain the polynucleotide and a method for decreasing flower, fruit, or leaf drop in a plant upon exposure to cethylene, comprises introducing the polynucleotide into a plant. The polynucleotide preferably comprises a nucleotide sequence encoding a cells mutant receptors). The regulatory nucleotide sequence comprises or ein4 mutant receptors). The regulatory nucleotide sequence comprises a comprise contain the polynucleotide sequence comprises a contain the polynucleotide, protein, and method are useful in decreasing mutant ethylene receptors present sequence represents plasmid plasmid plasmid plasmid method are useful in decreasing mutant ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide encoding a mutant plant ethylene receptor protein, useful in decreasing flower, fruit, or leaf drop in a plant upon exposure
                                                                                                                             Cotton; ethylene receptor; ds; ethylene insensitivity; abscission zone tissue; plant; transgenic; flower drop; fruit drop; leaf drop; EIN; ethylene insensitive; EIL; ethylene insensitive; lik; chitinase; cellulase; polygalacturonase; pLBS107; cyclic; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11606 BP; 3014 A; 2696 C; 2782 G; 3113 T; 0 U; 1 Other;
                                                                                      Plasmid pLBS107 expressing mutant ethylene receptor etrl-1.
                                                                                                                                                                                                                                                                                                                                                                                               /product= "mutant ethylene receptor etr-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor etrl-1 from the cotton chitinase promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 9; 59pp; English.
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1674. .3890
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2002; 2002US-0390385P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2003; 2003US-00602475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klee HJ, Lashbrook C,
                                                                                                                                                                                                                                           Gossypium hirsutum.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KLEE/) KLEE H J.
(LASH/) LASHBROOK C.
(SHRO/) SHRODE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-533137/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                             JS2004128719-A1
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                                                                                                                                                                                                                                                                                        Synthetic
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Length 11606;

Score 310; DB 12; Pred. No. 7.3e-28;

100.08;

Query Match Best Local Similarity

2299 TATTITITAATGCATITITATGACTIGCCAATTGATTGACAACATGCATCAATGGACTGC 2358

2359 AGCCACTCGA 2368

310

AGCCACTCGA

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translationally through the conversion of a conserved lysine residue by DHS. Also claimed are eIF-5A and DHS expression vectors for plant transformation and methods for modulating (inhibiting or increasing) eIF-5A or DHS expression in a plant. Inhibiting expression confers an increased resistance to virulent damage arising from pathogen ingression as compared to wild type plants. The methods and compositions of the particular for modulating (increasing/up-regular protein synthesis, in particular for modulating (increasing/up-regulating or inhibiting) the expression of eIF-5A and/or DHS, and for producing transgenic plants with modulated senescence, wounding and growth. The present sequence was used
                                                                                                                                                                                                                                                                               GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120
                                                                                                                                                                                                                                                                                                                                          GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYLCV, replication associated protein; Rep; transgenic plant; virus resistance; disease resistance; crop protection; PKYLX71:25S2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   CTCTTGTGTTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTTCCAGAATCCTTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATGGA 661
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                                                                                                                                                                                                       Length 662;
                                                                                                                                                                            Sequence 662 BP; 188 A; 97 C; 117 G; 260 T; 0 U; 0 Other;
                                                                                                                                                                                                                                    Indels
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/note= "duplicated 35S enhancer"
                                                                                                                                                                                                       Score 295; DB 14;
Pred. No. 6.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enhancer"
                                                                                                                                                                                             17.6%; Scor.
100.0%; Pred. No. o...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "duplicated 35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression cassette in PKYLX71:3582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type= TANDEM
/function= "Promot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomato yellow leaf curl virus. Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV76269 standard; DNA; 1998
                                                                                                                                                   to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537. .119u
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .863
                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 295; Conservative
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28-MAR-2003
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                                                             4307
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                                                                                                                                                                                                                                                                                             4547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isoforms of senescence-induced, wounding-induced and growth eukaryotic initiation Factor 5A (eIF-5A), for use in producing transgenic plants with modulated senescence, wounding and growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to eukaryotic initiation Factor 5A (eIF-5A) and deoxyhypusine synthase (DHS) sequences. eIF-5A is an essential protein factor which is involved in the initiation of eukaryotic cellular protein synthesis. It is characterised by the presence of hypusine [N-(4-amino-2-hydroxybuty1)lysine], which is formed on eIF-5A post-
                                                                                        120
                                                                                                                                                 180
                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                   300
                                  09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotic initiation Factor 5A; eIF-5A; plant; transgenic plant; crop improvement; plant breeding; plant disease; plant growth inhibitor; senescence; wounding; growth; ds.
                                                    TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                            GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                            crcrrcrcrrrragacarrrangaacrrrccrrrrargraarrrrccagaarccrrcrag
                                                                                                                                                                                                         ATTICTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA
                                                                                                                                                                                                                               ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAA
                                                                                                                                                                                                                                                                  TATTTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGACATCAATCGACCTGC
                                                                                                                                                                                                                                                                               TATTITITAATGCATTITIATGACTTGCCAATTGATTGACAACATGCATCGACCTGC
                                                                                          GGCAACAAATATATTTTCAGACCTAGAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                   CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTTCCAGAATCCTTGTCAG
                                 1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
      Gaps
      ö
    Indels
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eIF-5A wounding-induced related vector DNA.
      Mismatches
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; 2003US-0479969P.
; 2004US-0570833P.
; 2004US-0570835P.
; 2004US-00862440.
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      Conservative
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                                                                                                                                                                                                                                                                                                                           AGCCACTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2003;
20-JUN-2003;
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14-MAY-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson JE;
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      Matches
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The present sequence is that of luciferase expression vector ACT-OM-LUC comprising an expression construct composed of an actin 2 regulatory element comprising an enhancer and promoter, a tobacco mesaic virus omega translational enhancer, a nuclectide sequence encoding luciferase, and an RbcS E9 polyA region. Claimed vectors, including ACT-OM-LUC, can be used to transform a plant cell such that the cell expresses luciferase in an amount sufficient to produce at least 750,000 photons of visible light/sq mm/second. Also claimed are visibly bioluminescent transgenic plants that contain the genetically modified plant cell. The transgenic plant may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel genetically modified plant cell, useful as research tool, comprises a heterologous nucleotide sequence encoding a bioluminescent polypeptide expressed in an amount sufficient to produce visible light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3280 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a monocot or dicot, including an angiosperm, cereal, legume, oilseed plant or hardwood tree, or an ornamental plant such as petunia or carnation (all claimed). The transgenic plants are useful as research tools and have ornamental value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                            *tag= a
note= "region specifically referred to in Claim 21"
                                                                                                                                                                                                                            /*tag= c
/note= "tobacco mosaic virus omega translational
enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12304 BP; 2928 A; 3115 C; 3142 G; 3119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.3%; Score 289; DB 8; Length 12304;
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/*tag= b
/note= "actin 2 enhancer and promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "RbcS E9 polyA region"
                                                                                                                                                                                                                                                                                                                                                                'product= "Luciferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 90-96; 96pp; English.
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-2002; 2002WO-US011116.
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                        Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1883 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTTGAAG 1942
                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the nucleotide sequence of an expression cassette in PKYLX7135S2. The promoter in this plasmid is a 35S promoter modified by a duplicated enhancer region. The invention provides a means for producing virus resistance in tomato and other crops to infection by tomato yellow leaf curl virus-Israel (TYLCV-Is). A claimed method of providing resistance in a plant involves transforming the plant with a polynucleotide comprising a fragment of a TYLCV Rep gene, a polynucleotide antisense to the truncated Rep gene, or a polynucleotide truncated Rep gene or antisense sequence. The plant is selected from statice, petunia, lisianthus, tomatillo, and especially tomato or tobacco, and transformation is performed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1703 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1823 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 1882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                  Providing resistance to infection by a tomato yellow leaf curl virus in plant or plant tissue comprises transforming the plant or plant tissue with a polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTTCCAGAATCCTTGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1943 TATTTTTTATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGA 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector; ACT-OM-LUC; transgenic plant; bioluminescence; luminescence; firefly; luciferase; enzyme; plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agroinfection, biolistic targetting, electroporation or direct gene injection. (Updated on 27-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%; Score 295; DB 8; Length 1998;
100.0%; Pred. No. 5.6e-26;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1998 BP; 625 A; 411 C; 408 G; 554 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 40-41; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV75876 standard; DNA; 12304 BP
                                           07-MAY-2001; 2001US-0289315P.
07-MAY-2002; 2002WO-US014481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 295; Conservative
                                                                                                                                                            Polston JE, Hiebert E;
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Tobacco mosaic virus.
                                                                                      (POLS/) POLSTON J E. (HIEB/) HIEBERT E.
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Query Match

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RESULT 15 ABV75876 3339

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 Db
 3460 ATTCTAATCATTGCTTTATAATTATAGTTATGGTTTGTAGGATTTGTAGGTTGGGTATGAAA 3519

 Qy
 241 TATTTTTAATGCTTTTATGACTTGCCAATTGATGACATGCATC 289

 Db
 3520 TATTTTTTAATGCATTTATGACTTGCCAATTGATGACAGATGCATC 3568

Search completed: March 31, 2006, 06:51:52 Job time : 1110.43 secs

AJ925925 AJ925925

Title: Perfect score:

0

Sequence:

Scoring table:

Searched:

Database

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CK997149 ip15c02.b
CG75c0135 P044-3-D0
AG349657 Mus muscu
AJ516963 Arabidops
AL061936 Drosophil
CW952344 TCB38.1.D
AG347098 Mus muscu
CL068807 CH216-115
AL069706 Drosophil
AG350139 Mus muscu
AG350139 Mus muscu
AG350139 Mus muscu
CA94642 TCB34.3.D
AG340947 Mus muscu
CL139092 ISB1-1110
CL118721 ISB1-72J8
AG349719 Mus muscu
CL139092 ISB1-1110
CL118721 ISB1-72J8
AG349719 Mus muscu
CL139092 ISB1-110
CL139092 ISB1-110
CL139092 ISB1-1388
AG349719 Mus muscu
CL139993 AG340-612
CL033318 CG440-G12
CG757986 P053-2-D0
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CNS0021J
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AG347098
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CW949642
AG340947
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                           GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                      IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1675
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9b est6: *
9b est7: *
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9b gss2: *
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gb_est2:*
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AJ517160 Arabidops AJ517094 Arabidops AJ517095 Arabidops AJ517085 Arabidops AJ517065 Arabidops AJ517045 Arabidops AJ5171045 Arabidops AJ517113 Arabidops AJ516986 Arabidops AJ516980 Arabidops AJ516980 Arabidops AJ516980 Arabidops CG753083 P048-1-CO CK997149 ip15c02.b CG753083 P048-1-CO AJ517144 Arabidops CC353231 CH261-180 AJ925855 AJ925855 DN685273 CG26-G12 AG386981 Mus muscu CG757503 P052-4-C0 CG754863 P050-2-G0 Description SUMMARIES ATH517056
ATH517056
ATH517065
ATH517067
ATH517113
ATH51696
ATH51696
CG753083
CG753083
AG43010
ATH517144
CC253231
AJ925855
DM685273
CC262481 ATH517160 ATH516972 AG386981 CG757503 CG754863 07 Length DB Query Score 280 280 280 277.4 258.4 256 256 221.2 218.4 201 169.8 162.6 162.2 162.2 161.2 160.8 160.6 156.2 155.2 164.2 22109 22109 22109 22109 Š. Result

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10: 11:

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LOCUS	ATH517160 815 bp DNA linear GSS 22-NOV-2002
DEFINITION	sis thaliana GSS,
ACCESSION	
VERSION	1.091
KEYWORDS	
SOURCE	Arabidopsis thatland (thate Cress)
ORGANISM	Arabidopsis thallana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Itacheophyta;
	Spermatopnyta; Magnollopnyta; eudicotyledons; core eudicotyledons;
avivadaaaa	TOBLES; GUILOSILES II; DIASSICATES; DIASSICACEAE; ATALIACEES.
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REFERENCE	2 (bases 1 to 815)
AUTHORS	Reiss, B.
TITLE	Submission
JOURNAL	
	Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES	Location/Qualifiers
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	/ CIONG== Z2B/ / "
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ORIGIN	
Query Match	16.7%; Score 280;
 Best Loca Matches	Best Local Similarity 100.0%; Pred. No. 3.2e-29; Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	219 0.000
à À	
, Db.	153 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 212
e	
3	379 AGAATAATTTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTAT 438
Db 2.	213 AGAATAATTTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTAT 272
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Reiss, B.
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Arabidopsis thaliana GSS, clone 22B/469, genomic survey sequence.
AJ517094
AJ517094
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AJ517094.1 GI:25252831
GSS; genome survey sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                             499 AATTGGTAATTACTCTTTCTTTTTCTCCATATTGACCATCATACTCATTGCTGATCCATG 558
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An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
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                                                                                         559 TAGATTTCCCGGACATGAAGCCATTTACAATTGAATATAT 598
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16.7%; Score 280; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 280; Conservative 0; Mismatches 0;
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2 (bases 1 to 865)
Reiss, B.
Direct Submission
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ATH517056 1146 bp DNA linear GSS 22-NOV-2002
Arabidopsis thaliana GSS, clone 22B/820, genomic survey sequence.
AJ517056
                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 956)
Ichikawa, T., Rosso, M., Werber, M., Dekker, K., Schell, J. and Reiss, B. An Arabidopsis promoter activation-tagged flanking sequence
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1146)
Ichikawa, T., Rosso, M., Werber, M., Dekker, K., Schell, J. and Reiss, B.
An Arabidopsis promoter activation-tagged flanking sequence
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GSS; genome survey sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/organism="Arabidopsis th
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FEATURES

ATH516972 956 bp DNA linear GSS 12-MAR-2003 Arabidopsis thaliana GSS, clone 22B/658, genomic survey sequence. AJ516972.1 GI:25252596

DEFINITION ACCESSION VERSION

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ATH517067 796 bp DNA linear GSS 22-NOV-2002 Arabidopsis thaliana GSS, clone 22B/933, genomic survey sequence. AJ517067
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1 (bases 1 to 796)
Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B. An Arabidopsis promoter activation-tagged flanking sequence collection (AATSIC)
Unpublished
2 (bases 1 to 796)
Reiss,B.
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Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
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GSS; genome survey sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/db Xref="taxon:3702"
/clone="22B/933"
/ecotype="Columbia"
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863 bp DNA linear GSS 22-NOV-2002
Arabidopsis thaliana GSS, clone 22B/472, genomic survey sequence.
AJ517085
AJ517085.1 GI:25252813
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Unpublished
2 (bases 1 to 863)
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(bases 1 to 683)
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                                                                                                                                                                                                          26; Indels
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    .863
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db xref="taxon:3702"
/clone="22B/472"

                                                                                                                                                               Score 277.4; DB 1
Pred. No. 6.9e-29;
0; Mismatches 26
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
1. .1146
/organism="Arabidopsis th
/or_Lype="genomic DNA"
/db_xref="taxon:3702"
/clone="228/820"
/ecotype="Columbia"
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Best Local Similarity 91.8%;
Matches 293; Conservative
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ATH516966 970 bp DNA linear GSS 12-MAR-2003
Arabidopsis thaliana GSS, clone 22B/774, genomic survey sequence.
AJ516966
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 808)
Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
Unpublished
2 (bases 1 to 808)
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1 (bases 1 to 970)
1 Chikawa, T., Rosso, M., Werber, M., Dekker, K., Schell, J. and Reiss, B. An Arabidopsis promoter activation-tagged flanking sequence collection (AATSTC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 CAAAATGTACTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
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Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
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Pred. No. 4.2e-21;
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="caxon:3702"
/clone="22B/746"
/ecotype="Columbia"
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SCS; genome survey sequence.
Arabidopsis thaliana (thale cress)
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(bases 1 to 1601)

Ichkawa, T., Rosso, M., Werber, M., Dekker, K., Schell, J. and Reiss, B. An Arabidopsis promoter activation-tagged flanking sequence collection (AATSTC)
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      314 TAGATTTCCCTGACCAGAACCACCACGATGGAAATCGAAACAGACACAGATATCATCA 373
                                                                                                                                                                                   ATH517045 1601 bp DNA linear GSS 22-NOV-2
Arabidopsis thaliana GSS, clone 22B/83, genomic survey sequence.
AJ517045
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Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/mol_type="genomic DNa"
/db_xref="taonomic 3702"
/clone="22B/83"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                    GSS; genome survey sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Matches 274; Conserv
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                                               619 TAAC 622
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FEATURES

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Reiss, B.

RESULT 8

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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1895)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                    1896 bp DNA linear GSS 24-OCT-2003
P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
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                                                                                                                                         498 AAATTGGTAATTACTCTTTTTTCTCCATATTGACCATCATACTCATTGCTGATCCAT 557
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                                                                                                                                                               AAATTGG-GANCCCTCTTTTTTCTCCATATTGACCATCACACTCATTGCTGATCCAT 39
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                                                                                     TCAAATGGACCTTCTCTTTATAATAACGCTGCGGACATCTACANTTTTGTATTGAAAA
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                                                               TCAAAATGTACTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAAATAA
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/clone_lib="Pap BcoR! BAC Library"
/note="The Library was generated by a partial digest
the genomic DNA with EcoR! and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 4.4e-14;
0; Mismatches 449; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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                                                                                                                                                                                                                   GTAGATTTCCCGGACATGAAGCCATTTACA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                                                                                           Location/Qualifiers
1. 1896
/organism="Pristionchus p:
//ol_type="genomic DNA"
/stain="california"
                                                                                                                                                                                                                                                                                                                                                                                                                                CG753083.1 GI:37977199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pristionchus pacificus
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Best Local Similarity 50.2%;
Matches 457; Conservative
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Arabidopsis thaliana GSS, clone 22B/557, genomic survey sequence.
AJ516980
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                                                                                                                                                                                                                                                       260 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAAATT 201
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1 (bases 1 to 975)
                                                                                                                                                                                                                                                                                                          379 AGAATAATTTGTTTTTTTTTTTTTTTTAAATACGACGGATCGTAATTTGTCGTTTTAT 438
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Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
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1. .970
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/774"
/note="ecotype: Columbia"
                                                                                                                                                           DB 10;
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87.4%; Pred. No. 2.5e-18;
live 0; Mismatches 31;
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/mol_type="genomic_DNA"
                                                                                                                                                       Score 218.4; DB 1:
Pred. No. 9.8e-21;
0; Mismatches 7
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/db_xref="taxon:3702"
/clone="228/557"
/note="ecotype: Columbia"
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                                                                                                                                                     Query Match 13.0%;
Best Local Similarity 96.4%;
Matches 244; Conservative (
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Best Local Simil
Matches 236; (
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/tissue_type="Cerebellum"
/dev stage="3 month old normal canine"
/lab_host="XiJO Gold"
/lab_host="XiJO Gold"
/clone lib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site 1:
EcoR; Site 2: Xhol; Library constructed using pBluescript
KR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 169; DB 7; larity 49.1%; Pred. No. 6e-14; Conservative 0; Mismatches 56
                                                                                                     /organism="Canis familiaris"
/mol type="mRNA"
/db_xref="taxon:9615"
/clone="ip15c02"
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: ip15 row: c column: 02
High quality sequence stop: 1313.
Location/Qualifiers
                                                                                                                                                                        /sex="Unknown"
                                                                                     j. .1313
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Canis familiaris
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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ESTS from Canis familiaris cerebellum (dog)
Unpublished (2004)
Unpublished (2004)
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Tel: 516 367 8884
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Duery Match  9.8%; Score 164.2; DB 10; Length 1896;  Best Local Similarity 48.4%; Pred. No. 2.6e-13;  Matches 587; Conservative 0; Mismatches 613; Indels 13; Gaps  453 ATTITATAATAAAAATTAAATAATAAATAATAAAAAAAA	1420 866 1360 1360 1360 11240 11240 11240 11240 11240 11261 1120 1161 1161 1161 1161 1161 11	
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S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

L Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Taurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWG01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-6074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                          1581 TCTATTGAGCATATGTTTTAAACCAAGTAATGTTGAGTGCGGTAGTAAAACTCATTACAC 1640
                                                                                                                                                                                                                                                                                                                    AG430010 1227 bp DNA linear GSS 21-DEC-2004 Mus musculus molossinus DNA, clone:MSMg01-304N17.TJ, genomic survey
                1461 CTAAAAATAATATATCATACCAAAAAATTCTTAAAATGAATCTGATAATACTTAACCCC 1520
                                                                                                     Contribution of Asian mouse subspecies Mus musculus molossinus to appendic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
                                                                                                                                                                       1521 TITIATAAAACAATCTTAACCCCTTATATATTTTAATATTAATATATATAAATATAAA
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/clone Tib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus molossinus (Japanese wild mouse)
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/sub_species="molossinus"
/db_xref="taxon:57486"
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AG430010.1 GI:48073073
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Pred. No. 4.6e-13;
0; Mismatches 486;
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NITION Arabidopsis thaliana GSS, clone 22B/398, genomic survey sequence.

SSION AJ517144

AJ517144

GI:2525928

GSS; genome survey sequence.

RDS

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

ENATSM Arabidopsis thaliana

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Arabidopsis thaliana

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GOBERNATOR:

ARABICOPSI (Dases 1 to 820)

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COLECTION (AATSTC)

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Colection (AATSTC)

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Direct Submission
Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
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9.7%; Score 162.2; DB 10; Length 820;
Best Local Similarity 92.6%; Pred. No. 5.7e-13;
Matches 200; Conservative 0; Mismatches 13; Indels 3;
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ORGANISM
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ATH517144
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Search completed: March 31, 2006, 12:24:23 Job time : 7674.01 secs

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Patent No. 5428147
Sequence 11, Appl
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Sequence 15940, A
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2 6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*

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9: /cgn2 6/ptodata/1/ina/RB_COMB.seq:*

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US-09-434-039A-1

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US-09-434-039A-4

US-09-434-039A-4

US-09-098-219B-5

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US-09-9923-109-6

US-09-9923-109-6

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US-09-186-002-13

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Sequence 14164, A Sequence 9, Appli Sequence 9, Appli Sequence 17164, A Sequence 17145, A Sequence 17145, A Sequence 17145, A Sequence 12776, A Sequence 12776, A Sequence 1378, A Sequence 1378, A Sequence 1378, A Sequence 15348, A Sequence 15349, A Sequence 15350, A Sequence 15350, A Sequence 15507, A Sequence 15507, A Sequence 15509, A Sequence 15509, A		3; Length 8012; e-42; 0; Indels 0; Gaps 0; dGTTGTACCATTATGCTTATTCACTA 60 AGTTGTACCATTATGCTTATTCACTA 2767 CAAATGTTACTGAATACAAGTATGTC 120 CAAATGTTACTGAATACAAGTATGTC 2827 ATGTAATTTTCCAGAATCCTTGTCAG 180 ATGTAATTTTCCAGAATCCTTGTCAG 2887 CATGGATTTGTAGTTGAGTATGAAAA 240 CATGGATTTGTAGTTGAGTATGAAAA 240 CATGGATTTGTAGTTGAGTATGAAAA 240 CATGGATTTGTAGTTGAGTATGAAAA 240
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8.9 18773 3 8 8 7 11978 3 8 8 7 11978 3 8 8 7 11978 3 8 8 1 18773 3 8 8 1 18773 3 8 8 1 18773 3 3 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Pplication US 104436 10	Similarity 100.0%; 0; Conservative TGACCGAAGTTAATATGAC GGCAACAAATATTTTCA GGCAACAAATATTTTTCA GGCAACAAATATTTTTCA GGCAACAAATATTTTTCA CTCTTGTGTTTTTAGACATT CTCTTGTGTTTTTAGACATT CTCTTGTGTTTTTAGACATT CTCTTGTGTTTTTAGACATT ATTCTAATCATTGCTTTAI
25 149 2 2 146 2 2 2 146 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 US-09-182-117-1 Sequence 1, Appli Patent No. 620443 GENERAL INFORMAT APPLICANT: TITLE OF INVEN NUMBER OF SEQUENCHER: I OPERATING SY SOFTWARE: P SOFTWARE SOFTWARE TYPE: NUCLE STRANDEDNESS TYPE: NUCLE TYPE:	Ouery Match Best Local 8 Best Local 8 Matches 310 Oy 61 Ob 2768 Oy 121 Ob 2828 Oy 181

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2687 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA 2746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8418;
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.5%; Score 310; DB 3; 100.0%; Pred. No. 2.8e-42; ative 0; Mismatches 0;
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APPLICANT: MANNERLOEF, Marie APPLICANT: TERNING, Paul Peter; APPLICANT: TERNING, Per TITLE OF INVENTION: Transgenic Plants; TITLE OF INVENTION: Transgenic Plants; TITLE OF INVENTION: Transgenic Plants; PRICA RAPPLICATION NUMBER: US/09/434,039A; CURRENT FILING DATE: 1999-11-04; PRIOR FILING DATE: 1997-10-31; PRIOR APPLICATION NUMBER: 09/182,117; PRIOR FILING DATE: 1998-10-29; NUMBER OF SEQ ID NOS: 36; SOFTWARE: Patentin version 3.0; SEQ ID NO 5; SEQ ID NO 5; SEQ ID NO 5; TURNING DATE: 1998-10-29
                                                                                                                       FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8418 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 310; Conservative
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US-09-434-039A-5
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                               241 TATTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC 300
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18.5%; Score 310; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09434039A
Patent No. 6531649
GENERAL INFORMATION:
APPLICANT: MANNERLOEF, Marie
APPLICANT: STEEN, Per
ITLE OF INVENTION: Transgenic Plants
FILER REFERENCE: 09/444,039
CURRENT APPLICATION NUMBER: US/09/434,039A
CURRENT PILING DATE: 1999-11-04
PRIOR FILING DATE: 1999-10-31
PRIOR SEQ ID NOS: 36
NUMBER OF SEQ ID NOS: 36
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TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 6204436
GENERAL INFORMATION:
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US-09-434-039A-1
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Patent No. 6441277
GENERAL INFORMATION:
APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6441277dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
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Fatent No. 6531649
GENERAL INFORMATION:
APPLICANT: MANNERLOFF, Marie
APPLICANT: STEEN, Per
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 09/434,039
CURRENT APPLICATION NUMBER: 05/0112,03
FRICH FILING DATE: 1999-11-04
FRICH FILING DATE: 1999-11-04
FRICH FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 8798
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; ORGANISM: Sugar beet
US-09-434-039A-4
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US-09-434-039A-4
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                                       1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
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TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
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100.0%; Pred. No. 2.8e-42;
tive 0; Mismatches 0;
Mismatches
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 8798 base pairs
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Best Local Similarity 100.0
Matches 310; Conservative
Matches 310; Conservative
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STRANDEDNESS: double
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US-09-182-117-4
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TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic Pl FILE REFERENCE: 11899.0086.DVUS02 (MOBT:086-2)
CURRENT APPLICATION NUMBER: US/10/164,204
CURRENT APPLICATION NUMBER: US/00-06-06
PRIOR APPLICATION NUMBER: 09/098,219
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 6
SOFTMARE: PatentIn version 3.1
SEQ ID NO 5.
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Patent No. 6716474
GENERAL INFORMATION
APPLICANT: Barry, Gerard
Cheikh, No. 6716474dine
Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.5%; Score 310; DB 3; Length 10846; Best Local Similarity 100.0%; Pred. No. 2.8e-42; Matches 310; Conservative 0; Mismatches 0; Indels 0
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ZIP: 77210-4433
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/99/923,109
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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US-09-923-109-5
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     Aldolase in Transgenic Plants
                                                                                                                                                                                                                                                  MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,219B
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18.5%; Score 310; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kammerez, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 29,775
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
TITLE OF INVENTION: Aldolase in Trans NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: TX
COUNTY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
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APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6663906dine; APPLICANT: Kishore, Ganesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:

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                                                                                                                                  NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 29,775
RELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER.STICS:
LENGTH: 10900 base pairs
TYPE: mucleic acid
STRANDENESS: double
      US/09/098,219B
                      FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-UTM-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10164204; Patent No. 6663906; GENERAL INFORMATION:
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Matches 310; Conservative
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      APPLICATION NUMBER:
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TOPOLOGY:
US-09-098-219B-6
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Patent No. 6441277
GENERAL INFORMATYON:
APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6441277dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
TITLE OF INVENTION: Aldolase in Transgenic Plants
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PIP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             18.5%; Score 310; DB 3; I
100.0%; Pred. No. 2.8e-42;
tive 0; Mismatches 0;
                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION:
TELEPHONE: 713-787-1400
APPLICATION NUMBER: 09/098,219
PLILING DATE: «Unknown»
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-UNN-1997
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                    LENGTH: 10846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                               TELEFAX: 713-787-1440 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6663906dine
APPLICANT: Cheikh, No. 6663906dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic P
FILE REFERENCE: 11899.0086.DVUS02 (MOBT:086-2)
CURRENT APPLICATION WUMBER: US/10/164,204
CURRENT FILING DATE: 2002-06-06
PRIOR PILING DATE: 1998-06-16
NUMBER: OF 097089,219
NUMBER: OF 097089 05-16
SOFTWARE: Patentin Version 3.1
SEQ ID NO 6 2118 2178 ö 2179 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 2238 2239 ATTCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA 2298 2299 TATTITITAATGCATTITATGACTTGCCAATTGACAAGACATGCACATGCATCAATTGC 2358 240 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTTCCAGAATCCTTGTCAG 180 TATTITITAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC 300 2059 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACTTGTCATTATGCTTATTCACTA 2119 GGCAACAAATATATATCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 181 AITCTAATCATTGCTTTATAATTATAGTTATACTCATGGATTTGTAGTTGAGTATGAAAA 1 TGACCGAAGTTAATATGAGGAGTAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA Gaps ö 18.5%; Score 310; DB 3; Length 10900; ; OTHER INFORMATION; P-FMV/CTP2/fda/NO3' US-10-164-204-6

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Gaps

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2179 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG 2238
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APPLICANT: Rhoads, David M
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
FILE REFERENCE: UNL2990
CURRENT FALPICATION NUMBER: US/09/577,424
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                    2059 TGACCGAAGTTAATATGAGGAGTAAAAACACTTGTAGTTGTACCATTATGCTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                   GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                           2119 GCCAACAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
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                                                                                                                                             Length 10900;
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                                                                                                                                                                                                       Indels
                                                                                                                                             Query Match
18.5%; Score 310; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0;
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ORGANISM: Bacterial Plasmid DNA - Plasmid pZP-ALE
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17.3%; Score 289; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 289; Conservative 0; Mismatches 0;
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                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09577424
; Patent No. 6525245
STRANDEDNESS: double
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US-09-577-424-1
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US-09-923-109-6
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                                                                                         Gaps
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Cheikh, No. 6716474dine
Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
Aldolase in Transgenic Plants
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                           Length 10900;
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/923,109
FILING DATE: 06-Aug-2001
CLASSIFCATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/098,219
FILING DATE: CURNOWN>
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Assertice and Application and Application Applicatio
                                                                                  Indels
                        Query Match
18.5%; Score 310; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
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ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
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TYPE: nucleic acid
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TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09923109
Patent No. 6716474
GENERAL INFORMATION:
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2739 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 2798
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LOCATION: 484..684
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
FORTHER: CDS
LOCATION: complement (729..1340)
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                   COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verson #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 16 JANUARY 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVERSENSON, LEGONARD R.
REGISTRATION NUMBER: 30,330
REPERENCE/DOCKET NUMBER: 2.21-0111P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
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OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
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OTHER INFORMATION: /note= "T-DNA left border
OTHER INFORMATION: sequences"
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LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
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OTHER INFORMATION: /label= 35S promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
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3882 AITCTAATCATTGCTTTATAATTATACTTATACTCATGGATTTGTAGTTGAAGA 3941
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APPLICANT: Wang, Qi
APPLICANT: Dubois, Patrice
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof
FILE REPRENCE: 13587.106
CURRENT APPLICATION NUMBER: US/10/015,637
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/255879
PRIOR APPLICATION NUMBER: US 60/255879
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
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Patent No. 5962768
GENERAL INFORMATION:
APPLICANT: CONNELLSEN, MARCUS
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: VAN AARSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES: 6
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Patent No. 6927321
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Best Local Similarity 100.0
Matches 282; Conservative
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US-10-015-637-7
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/ cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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US-11-057-062-2
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OTHER INFORMATION: recombinant DNA construct in plasmid between Agrobacterium OTHER INFORMATION: borders
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                                3437 AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA 3496
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US-11-057-062-2/c
| Sequence 2, Application US/11057062
| Sequence 2, Application US/11057062
| Publication No. US20050176670A1
| GENERAL INFORMATION:
| APPLICANT: Malvar, Thomas
| APPLICANT: Hunethy, Michael
| TITLE OF INVENTION: Recombinant DNA for Gene Suppression
| TITLE OF INVENTION: Recombinant DNA for Gene Suppression
| CURRENT PEPLICATION NUMBER: US/11/057,062
| CURRENT FILING DATE: 2005-02-10
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: PatentIn version 3.2
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Pred. No. 2.1e-28;
0; Mismatches 12; 1
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96.4%;
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Best Local Similarity 96.4
Matches 320; Conservative
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LENGTH: 7794
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                                                             <u>AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA</u>
                                                                                    AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10376763A
; Squence 5, Application US/10376763A
; Publication No. US20040172669A1
; GENERAL INFORMATION:
    APPLICANT: KWS SAAT AC
; TITLE OF INVENTION: Glyphosate tolerant sugar beet
    TILE REPERENCE: KWS-H7-1
; CURRENT APPLICATION NUMBER: US/10/376,763A
; UNMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Matches 592; Conservative
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                                                                                                                                             Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic Plants
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                                                                                                                                                                                                                                                                                                                             ZIP: 77210-4433

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATE:
    APPLICATION NUMBER: US/09/923,109
    FILING DATE: 06-Aug-2001
    CLASSIFICATION: <Unknown>
                                                                              APPLICANT: Barry, Gerard
Cheikh, No. US20020138875Aldine
Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/098,219
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-UN*-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Parricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
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TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 5:
                   Sequence 5, Application US/09923109
Patent No. US200201318875A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard
                                                                                                                                                                                                                                               STREET: P.O. Box 4433
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US-09-923-109-5
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Bisphosphate Aldolase in Transgenic P
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Publication No. US20040073976A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Cheikh, Nordine
APPLICANT: Kishore, Ganesh of Fructose 1,6 Bisphosphate Aldolase in Transgenic TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic TITLE OF INVENTION: Plants
FILE SERERELS CNUSO3 (MOBT: 086-3)
CURRENT APPLICATION NUMBER: US/10/705,430
CURRENT FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: 09/098,219
PRIOR APPLICATION NUMBER: 09/098,219
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                                                                                                                                                                                             Sequence 5, Application US/10164204
; Publication No. US20030126641A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard
; APPLICANT: Cheikh, No. US20030126641A1dine
; APPLICANT: Cheikh, No. US20030126641A1dine
; APPLICANT: Cheikh, No. US20030126641A1dine
; TITLE GOF INVENTION: Expression of Fructose 1,6 Bis;
; TITLE REFERENCE: 11899.0066.DVUS02 (MOBT:086-2)
; CURRENT PILION DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/098,219
; CURRENT FILING DATE: 1998-06-16
; NUMBER: OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: P-FMV/CTP1/fda/NOS3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 310; Conservative
2359 AGCCACTCGA 2368
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APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. US20030126641Aldine
APPLICANT: Cheikh, No. US20030126641Aldine
APPLICANT: Cheikh, No. US20030126641Aldine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic Pl
FILE REFERENCE: 11899.0086.DVUS02 (MOBT: 086-2)
CURRENT APPLICATION NUMBER: US/10/164,204
CURRENT APPLICATION NUMBER: 09/098,219
PRIOR APPLICATION NUMBER: 09/098,219
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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18.5%; Score 310; DB 6; L
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 310; Conservative 0; Mismatches 0;
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION INFORMATION:
TELEFHONE: 713-787-1440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10900 base pairs
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
TYPER: NUCLEIA CALL
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; OTHER INFORMATION: P-FMV/CTP2/fda/NO3'
US-10-164-204-6
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Publication No. US20030126641A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 310; Conservative
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Patent No. US20020138875A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard
Cheikh, No. US20020138875A1dine
Kishore, Ganesh
TITLE OF INVENTION: Andelase in Transgenic Plants
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                                                                                                                                                                                                                                                                                   Length 10846;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                 Query Match
18.5%; Score 310; DB 7; I
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 310; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/09/923,109
FILING DATE: 06-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/098,219
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: TX
                                                                                                                                                                                                        ) OTHER INFORMATION: P-FMV/CTP1/Eda/NOS3
                          NUMBER OF SEQ ID NOS: 6
SOFWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 10846
                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  PRIOR FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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US-09-923-109-6
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Sequence 9, Application US/10602475A

Sequence 9, Application US/10602475A

Publication No. US20040128719A1

GENERAL INFORMATION:

APPLICANT: Heac, Harry J.

APPLICANT: Lashbrook, Coralie

APPLICANT: Shrode, Lori

TITLE OF INVENTION: Insensitivity in Transgenic Plants

TITLE OF INVENTION: Insensitivity in Transgenic Plants

TITLE OF INVENTION: US-325XC1

CURRENT APPLICATION NUMBER: US/10/602,475A

CURRENT PILING DATE: 2003-06-23

PRIOR FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.2

SEQ ID NO 9

LENGTH: 11606

TUBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.2

SEQ ID NO 9

LENGTH: 11606
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; Publication No. US20050125862A1
; GENERAL INFORMATION:
; APPLICANT: Polston, Jane E.
; APPLICANT: Hiebert, Ernest
; TITLE OF INVENTION: Materials and Methods for Producing Tomato Yellow Leaf Curl Viru; TITLE OF INVENTION: Resistance in Plants
  2299 TATTTTTAATGCATTTTATGACTTGCCAATTGATTGACAACATGCATCAATCGACCTGC 2358
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OTHER INFORMATION: plasmid construct encoding mutant ethylene receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 310, Conservative
                                                                            2359 AGCCACTCGA 2368
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                                                   301 AGCCACTCGA 310
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LOCATION: (1674)..(3890)
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US-10-602-475A-9
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US-10-705-430-6

Sequence 6, Application US/10705430

Publication No. US20040073976A1

GENERAL INFORMATION:

APPLICANT: Barry, Gerard

APPLICANT: Kishore, Ganesh

TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic

TITLE OF INVENTION: Diants

TITLE OF INVENTION: Diants

FILE REFERENCE: 11899.0086.CMUS03 (MOBT:086-3)

CURRENT APPLICATION NUMBER: US/10/705,430

CURRENT APPLICATION NUMBER: 10/164,204

PRIOR PRILING DATE: 2003-11-11

PRIOR FILING DATE: 1998-06-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.2

SEQ ID NO 6

LENGTH: 10900
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                                                                       GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                      2119 GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
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18.5%; Score 310; DB 7; L
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: P-FMV/CTP2/fda/NO3'
US-10-705-430-6
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| Sequence 5. Application US/10473945
| Publication No. US20050081268A1
| GENERAL INFORMATION:
| APPLICANT: THE SCRIPPE RESEARCH INSTITUTE
| APPLICANT: Kuhlmann, Tina
| APPLICANT: Kuhlmann, Tina
| APPLICANT: Lerner, Richard A. TILLE OF INVENTION: BIOLUMINESCENT PLANTS AND METHODS OF MAKING SAME
| TILLE OF INVENTION: BIOLUMINESCENT PLANTS AND METHODS OF MAKING SAME
| FILE REFERENCE: SCRIP1340-1 | CURRENT FILING DATE: 2003-10-03 |
| PRIOR PLICATION NUMBER: US 60/282,094 |
| PRIOR PLICATION NUMBER: US 60/282,094 |
| PRIOR FILING DATE: 2001-04-06 |
| NUMBER OF SEQ ID NOS: 5 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 5 |
| TENTY: LENTY:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCAACAAATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
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17.3%; Score 289; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 289; Conservative 0; Mismatches 0;
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17.6%; Score 295; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 295; Conservative 0; Mismatches 0;
FILE REFERENCE: POL-100XCI
CURRENT APPLICATION NUMBER: US/10/477,240
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 60/289,315
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 1998
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US-10-473-945-5
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                                                               61 GGCAACAAATATTTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC 120
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APPLICANT: Kuhlmann, Tina
APPLICANT: Kuhlmann, Tina
APPLICANT: Kuhlmann, Tina
APPLICANT: Lerrer, Richard A.
TITLE OF INVENTION: BIOLUMINESCENT PLANTS AND METHODS OF MAKING SAME
FILE REFERENCE: SCRIP1340-1
CURRENT PAPLICATION NUMBER: US/10/473,945
CURRENT FILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 12497
                                                                                                                 3340 GCCAACAATATATTTTCAGACCTAGAAAAGCTGCAAATGTTACTGAATACAAGTATGTC
                                                                                                                                                                                             121 CTCTTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAATCCTTGTCAG
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17.3%; Score 289; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 289; Conservative 0; Mismatches 0;
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Publication No. US20050081268A1
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
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RESULT 14 US-10-015-637-7

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                                                                                         APPLICANT: Liang, Juhong
APPLICANT: Oulmassov, Tim
TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof
FILE REFERENCE: 13587.106
CURRENT APPLICATION NUMBER: US/10/015,637
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/255879
PRIOR FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof FILE REFERENCE: 13587.106
CURRENT APPLICATION NUMBER: US/11/148,661
CURRENT FILING DATE: 2005-06-09
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Pred. No. 6.5e-25;
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Application US/10015637
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Publication No. US20050241018A1
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SEQ ID NO 7
LENGTH: 632
                  US20030046727A1
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APPLICANT: Dubois, Patrice
APPLICANT: Liang, Jihong
APPLICANT: Oulmassov, Tim
                                                         APPLICANT: Wang, Qi
APPLICANT: Dubois, Patrice
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Best Local Similarity 100.
Matches 282; Conservative
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; ORGANISM: Pisum sp.
US-11-148-661-7
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ORGANISM: Pisum sp.
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/mol_type="unassigned DNA"
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Sequence 4 from Patent WO2004072235.
CQ860281
CQ860281.1 GI:51982087
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AL136380 Human DNA
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AC094221 Rattus no
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BV595271 S215P6122
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            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listello, J.J., Martens, A.B. and Sammons, B.
Cotton event mon 88913 and compositions and methods for
detectionthereof
L Patent: WO 2004072235-A 4 26-AUG-2004;
Monsanto Technology LLC (US)
Location/Qualifiers
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//note="taxon:32630"
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//note="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijishita,S., Honda,M., Ichikawa,Y.,
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Ito,Y., Iwabuchi,A., Kamiya,K., Karasawa,W., Katagiri,S.,
Kikuta,A., Kobayashi,T., Mukai,Y., Nagasaki,H., Nakashima,M.,
Nakama,Y., Nakamichi,Y., Nakamura,M., Namiki,N., Negishi,M.,
Ohta,I., Ono,N., Saji,S., Sakai,K., Shibata,M., Shimokawa,T.,
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Teulji,K., Waki,K.,
Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1

Jana, Jana, Jana, Jala,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Authorited (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (R-mail:tsasaki@nias.affrc.go.jp, WEL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Apr 16, 2002 this sequence version replaced gi:15146361.
Genes were predicted from the integrated results of the following: GRNSCAN (http://CR-081.mit.edu/GENSCAN.html), FGENESH (http://cpal.biology.gatech.edu/Genewark), GlimmerM (http://opal.biology.gatech.edu/Genewark), GlimmerM (http://poln.biology.gatech.edu/Genewark), GlimmerM (http://poln.biology.gatech.edu/Genewark), GlimmerM (http://poln.biology.gatech.edu/Genewark), GlimmerM (http://poln.craf.co.jp/RiceHMM/), SplicePredictor (http://poln.craf.psc.iastate.edu/cgl-bin/sp.cgl), sim4 (http://globin.cse.psu.edu/htm/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmerm/), BlaSTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein
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AP003258 BA000010
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Mismatches 0;
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16137. 17849
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alcohol/phenylethanol benzoyltransferase; BPBT"
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| Exref="G1:20160662"
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/note="start and end point are not identified"
complement(join(3771. .3823,5359. .5470))
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/note="hypothetical ORF
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/gene="P0463A02.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="P0463A02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="P0463A02.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="P0463A02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6137. .17849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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FRSPRAPSFSBAPARCLPSBPDRRHALLCTPRDRERD"
Complement (20127. 21140)
/gene="P0463A02.6"
/gene="P0463A02.6"
/note="P0463A02.6"
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GLLVYRGGOPPAPCYRDNDPSGIIRAALSRALVHYYPLAGRILREVEGRKLVIDCSGGG
VVYWEADANDYRLEBWRAAAAGGHGIRPSFPCYDQLVPDVRSSGRGGSYLSCPLVGIQV
TRLLCGGFIVGTAVNHSVCDAMGIVQFLINAVADIAGGLPAPAVHATWSRELLDARSPP
APAPPHREYDMIDILPGGGREADNIYRSFLFSSTDIAALKEBALLEPHEHRLGGGSST
ATSFEVLAAFLWRARTAALEVPADEEVRLVAVVGFSRIAALGLPSGYYGNTCAYPTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALHLLTSDLAAASGNTGGGVAVAVVDCLQFAMFSLLTYMCFGKRLDRRGVREIEAVO
RELESSYFREPVFAFCPFYKRLFPRRWQKVLSTRRQQEIPLEJLEISERKRKRIKISSM
DNDGSWCCYVDTI SHKLPKRAGDRRLTDGELVSLCTEFLTASVDTI VTALOMIMAR
VVEQPEIQAKLLDEINRVVSSDKEHVDEEDIKSMAYLKALVLEGLRRHPPAHFLLSHA
                                                                                                                                            MTAGELLKGCTLGDVVRLVQEAKAAVTAEYVRSTAECLVLRRRPRLARTNLFVVTDVR
RVGFDRVDFGWGDPVYGGPARALPTVSLLVNVKGSSNVVGAVVSLPSLVMGRFSAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="probably inactive due to including stop codon(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative cytochrome P450"
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|/translation="MEVILLPLVVIITSTMLLLLIISTAKKRHHGTANLPLPPAPPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVVGPLLMLVRARSNLEPAIRELHRRHGPILSLTFLSPRAAIFVSSREVTHRALVQRG
HTFASRPPAIAPFAVLTSGQCTVSSAPYGPLWRSLRRNLTSGVLGHGSRAPLYAPARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22720. .24042
/gene="P0463A02.7"
/note="probably inactive due to 3' exon missing in CDS
pseudogene, contains similarity to Zea mays
retrotransposon Opie-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                         /note="start and end point are not identified"
complement(19981. .20577)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="start and end point are not identified" 36588. .38162 /gene="P0463A02.10"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                     /gene="P0463A02.5"
complement(<19981. .>20577)
/gene="P0463A02.5"
                                                                                                                                                                                                                             .20577)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0463A02.8"
25112. .28140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22720. .24042
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                                                                                                                                                                                                                             complement (19981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bource
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Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y.,
Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K.,
Chiden,Y., Hayashi,M., Okancto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijishita,S., Honda,M., Ichikawa,Y.,
Idonuma,A., Injima,M., Ikeda,M., Ikeno,M., Ito,S., Ito,T., Ito,Y.,
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Nakama,Y., Nakamichi,Y., Nakamira,W., Namiki,M., Nagishi,M.,
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Tsuji,K., Waki,K.,
Yamagata,H., Yamane,H., Yokaki,K., Yoshihara,R., Yukawa,T.,
Yamagata,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1914/4938

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (20-JUN-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

On May 22, 2002 this sequence version replaced gi:14625024.

Genes were predicted from the integrated results of the following:
GENSCAN (http://CRR-081 mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.htm

(http://www.softberry.com/), GeneMark.htm

(http://www.iigr.org/tdb/glimmerm/glmr_form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RaceHMM), SplicePredictor

(http://pioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://pioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://pioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://pioinformatics.iastate.edu/cgi-bin/sp.cgi) and the cDNA

Genomic sequence was searched against NCBI NonRedundant Protein database

with BlansTP. BSTS represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no. and RGP clone ID.

Pull-length cDNAs represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no.
AVEETSLDGHRIPAGRSVNPSVADVAHDENVWSRPEEFLPERFLDGGEGAGTDLTGSR
EIKWMPFGVGRRICPGLGLALLQLEYFVANNVREFEWGMVDGDCGGGINLAERPEFTV
IMEQPLRALVVPRRRE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC clone:BIO51810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                        Length 151041;
                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                           Score 20; DB 15;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                    0; Mismatches
                                                                                       complement (38560. .41960)
/gene="P0463A02.11"
                                                                                                                                                                                                                                                                                                                                       3308 TTGAATATATATACAAAGC 3327
                                                                                                                                                                                                                                                                                       1 TTGAATATATATACAAAGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP003764 BA000010
AP003764.3 GI:21104808
                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
AP003764
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein'. A gene without significant homology to any protein but with full-length cDN or sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene prediction program is classified as a probable 'hypothetical' protein and is included as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
                                                                                                                                                                                                                                                                                                                                            The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of B1051B10 clone has an overlap with P0440D10 (DDBJ: AP003852) clone at 5' end and with P0463A02 (DDBJ: AP003258) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation='wasskpillgillsittcluoullaaanpopppppscDksdKelr
Pursowmarkakivscheegerkryowkgnthrigapregtollssgvgarprotitibs
VuganrrediltstervqptternasgfhsppttpisphswpptcvDwrssgavtgvkf
GVNCASGWAFAAAaleGLHKITTGELYSLSEQWWPDCDTGSFGCSGGHSDTALLVA
SRGGITSERKYPYTVGQSCDVGKLLPDHSASVSGFAAVPPNDRRQLALAVARQDVTV
YIDASAQBEQFYKGGVYKGFCNPGSVNHAVIIVGYCENFGGEKYWIAKNSWSNDWGEQ
GYVYLAKDVWWPQGTCGLATSPFYPTV"
Join (5111. 6135,18994. 19986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="probably inactive due to no initiation codon in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="probably inactive due to insertion of genes in CDS
pseudogene, RIM2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="contains EST(s): AU083497(R3689), AU032203(R3689)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inactive due to 5' exon missing in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<20778. :20839,20980. .>21409))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(<2444. .2936,3029. .>3621)

gene="B1051B10.1"

fnote="Btart and end point are not identified"

fnote="Btart and end point of identified"

form(2444. .2936,3029. .3621)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="putative SAG12 protein"
protein id="BAB93394.1"
db xref="G1:21104809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5131. .6135,18994. .19986)
/gene="B1051E10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative orf3 of RIRE2"
complement(11679, .14729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(7798. .9059,9459. .11034)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="B1051B10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .21409)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2444. .3621
/gene="B1051E10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="B1051E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (20778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .207782
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CDS

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Still Goggaelli, Rilbonces, Abramacon, S., Addms, C., Alder, J., Alden, H., Alsprooks, S., Admin, A., Angulano, D., Anguales, Maraie, Merzker, Lee., Abramacon, S., Addms, C., Allen, H., Alsbrooks, S., Annin, A., Angulano, D., Angualesechi, V., Angual, A., Ayogali, M., Baraneted, M., Benahmed, F., Blandshohus, D., Bandstanaike, D., Barber, M., Barsen, B., Benahmed, F., Blandshohus, D., Bandstanaike, D., Barber, M., Barsen, B., Benahmed, F., Blandshohus, D., Bandstanaike, D., Barber, M., Barsen, B., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chan, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chen, R., Din, H., Dayan-Chia, S., Dermon, S., Molly, S., M., Mand, S., L., Mand, S., Lews, J., M., Mand, S., M., Harlak, P., Harlak, P., Hand, S., Liu, S., Man, S., Man, S., Melly, S., Kally, S., Molly, S., Mo
                                                                                                                                                                                                                                                                                                                 AC130943 143780 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-410L18, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               AC130943.3 GI.25138999
HTG; HTGS_HASEZ; HTGS_BART; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
   Pred. No. 1.5e+02; Mismatches 0;
                                                                                            1 TTGAATATATATACAAAGC 20
1 Similarity 100.0%; Pr
20; Conservative 0;
Best Local &
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                     RESULT 6
AC130943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical ORF predicted by GlimmerM this category is not included in IRGSP standard" this category is not included in IRGSP standard" join (22943. 23072,23161. .23208,23291. .23895,23973. .24410. .25340,25423. .25575,25673. .25952,26371. .26454,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Bl051E10.8"
join(22943. .23072,23161. .23208,23291. .23895,23973. .24434,
24610. .25340,25423. .25575,25673. .25952,26371. .26454,
26869. .26925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(<28374. .28465,28581. .28650,28769. .>28924))
/gene="B1051E10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .32125,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="start and end point are not identified"
complement(join(28374. .28465,28581. .28650,28769. .28924))
/gene="B1051E10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MATVSQKLGDCGDCGASAQAHGQRGRRRHGRISAVARELVRAVD
LDPSSTQTLCMIVAATTRPKADNPGPMFIPPVDIVGSGKLDMEDHLFRTSTPIHHSSS
                                                                                                                                                                                                                                                                                   /trānslation="MDGRRQTHEGGGGDGGGEVEAAVVVEMATERVAVVGDPGVVEV
KAAGVVDPGVGEVGVGEVGGVVDLGRTAERTSGGGGEEGVEGGREGGGERQRWREGVE
VGVEGGGGGGGGGGGGEGSGEVEAATVERRAERARRGWRRWRGRESGAVTGEVTCDGLTVRA
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ATKPSVAAIDGLALGGGGTGALBANACHAR SIPTPAGLGLEALGGVI DEGGGTGRLDRLV
GLTKALEMMLLSKPIKGAEAHQLGLVDSLVSADDLVNTARRMALDICELKRPRTKSLY
KTDKLEPLGEAREILKPARAQARRQAANLEHPLVCIDVIEEGIVSGPRAGLWKEANAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MAAAAAKGRTEMEVGADGVAVITICNPPVNSLSIDVLLSLKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains EST(s): AU063400(C61341),AU085835(C61341)
contains full-length cDNA(s): AK10044,AK062168,AK099063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product = "putative tetrafunctional protein of glyoxysomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Bl05IE10.10"

join(30450. 30774,31708. 31779,31905. .31970,32069. .32

32219. .32286,32370. .33451,32747. .32802,32947. .33249,

33344. .33430,33501. .33675,33783. .33904,33991. .34154,

34227. .34481,34614. .34735,34844. .34965,35413. .35561,

35648. .35786,36017. .36329)
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join(30666. 30774,31708. 31779,31905. 31970,32069. 33
32219. 32286,32370. 32451,32747. 32802,32947. 33249,
33344. 33430,33501. 33675,33783. 33904,33991. 34154,
34227. 34481,34614. 34735,34844. 34965,35413. 35561,
//gene="Bl051E10.10"
/gene="B1051E10.6"
/note="start and end point are not identified"
complement(join(20778. .20839,20980. .21409))
/gene="B1051E10.6"
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                                                                                                                              note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="B1051E10_7"
join(21457. .21569,22350. .22440)
/gene="B1051E10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                    oin(21457. .21569,22350. .22440)
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complement (28374. .28924)
/gene="B1051E10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="hypothetical protein"
protein_id="BAD53839.1"
db_xref="G1:53792805"
                                                                                                                                                                                      product="hypothetical protein"
protein id="BAD53838.1"
db_xref="G1:53792804"
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db xref="GI:21104813"
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CDS

CDS

DB 15; Length 207782;

100.0%; Score 20;

Query Match

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                                                                                misc feature
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AUTHORS
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VERSION
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JOURNAL
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SOURCE
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AL355991
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                                                                                                                                                                                                                                                                            Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON Nov 20, 2002 this sequence version replaced gi:23908408.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads of the clome and there may be sequence contigs within a scottig-scaffold that consist entirely of whole senome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 143780: contig of 143780 bp in length.

Location/Qualifiers

| I. 143780: contig of 143780 bp in length.

| Corganism="Rattus norvegicus" |
| Ab_xref="genomic DNA" |
| Ab_xref="genomic DNA" |
| Ab_xref="taxon:10116" |
| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dases 1 to 143780).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1037
/note="wgs_end_extension
clone_end:T7"
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/note="wgs_end_extension
clone_end:T7"
2 (bases 1 to 143780)
Rat Genome Sequencing Consortium.
Direct Submission
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/note="clone_boundary
clone_end:T7
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                                        AUTHORS
                                                                                                      JOURNAL
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   REFERENCE
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HTG 10-JUL-2001
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AL355991. 5 G1:9800917
HTG; HTGS PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-UUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
gi:10280883, gi:9213695.
Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4, version 4.5 Sequencing vector: plasmid; 108752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 138717 bases at least Q40 Consensus quality: 141163 bases at least Q30 Consensus quality: 142550 bases at least Q20 Insert size: 144369; sum-of-contigs Insert size: 184369; vam-of-contigs Insert size: 180875; 7.0% error; agarose-fp Quality coverage: 3.80x in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 14; Length 143780;
Pred. No. 4e+02;
0; Mismatches 0; Indels 0;
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134792..136777
/note="wags end extension
clone end:Sp6"
137952..140046
/note="wags end extension
clone end:Sp6"
141598..143780
/note="wags end extension
clone end:Sp6"
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Center project name: bA149G23
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 100.0%; Partches 19; Conservative 0;
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us-10-541-346-2.rge

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Homo sapiens chromosome 1 clone RP11-102H4, 19 unordered pieces.
AL611928
AL611928.7 GI:160713747
HTG; HTGS PHAREI; HTGS_CANCELLED.
Homo sapiens (human)
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 11, 2001 this sequence version replaced gi:16030263.
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95.0%; Score 19; DB 14; Length 146469;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indel8 0;
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TITLE
JOURNAL
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AL611928
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AL136380 171656 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RP5-88207 on chromosome 1p33-34.2
Contains the 5' end of the PTCH2 gene for patched homolog 2
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100.0%; Pred. No. 3.7e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                               Assembly program: XGAP4; vergion 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 166102 bases at least Q40
Consensus quality: 166899 bases at least Q40
Consensus quality: 167607 bases at least Q20
Insert size: 168341; sum-of-contigs
Insert size: 18481; sum-of-contigs
Quality coverage: 7.77x in Q20 bases; sum-of-contigs Quality
coverage: 7.49x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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37643: contig of 29960 bp in length
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80295: contig of 8740 bp in length
7759: gap of 100 bp
80295: contig of 8740 bp in length
------ Genome Center
Center: Wellcome Trust Sanger Institute
                                                                                                       Contact: humquery@sanger.ac.uk
------- Project Information
Center project name: bA157D21
                                                                          Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                 --- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequesteseanger.ac.uk clonerequestes: clonerequesteseanger.ac.uk

On Feb 28, 2002 this sequence version replaced gi:18857781.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, FMEL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.aanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl

RP5-88207 is from the library RPCI-5 constructed by the group of Pieter de Jong. Por further details see that http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
(Drosophila), a ribosomal protein S2 (RPS2) pseudogene, the EIF2B3 gene for eukaryotic translation initiation factor 2B subunit 3 gamma 58kDa, a chromosome 14 open reading frame 18 (Cl4Orfil8) pseudogene, a peptidylprolyl isomerase A (cyclophilin A) (PPIA) pseudogene, a mitochondrial ribosomal protein S17 (MRPS17) pseudogene and four CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .17517),
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                      ALIJ6380.22 GI:19031310
HTG; C14orf18; CpG island; EIF2B3; MRPS17; patched; PPIA; PTCH2;
RPS2.
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oin(complement(2001. .18541),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.
1 (bases 1 to 171656)
Phillimore, B.
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Homo sapiens
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complement (1A.592166.16;9077. 97413),
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cambridgeshire, CBIO 15A, W. E. mail enquiries:
    Lumquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk
    numquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk
    numquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >=
    30); an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one Mi3 subclone; and the
    assembly was confirmed by restriction digest. The following
    abbreviations are used to associate primary accession numbers given
    in the feature table with their source databases: Em; EMBL; Sw;
    SWISSRROT; Tr:, TREMBL; Wp;, WORMPEP; Information on the WORWBEP

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1 (bases 1 to 215043)

Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-335N15 is
from the RCCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                            Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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  Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://mrcseq.har.mrc.ac.uk
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Rattus norvegicus clone CH230-2P14,
2 unordered pieces.
AC094221
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    117264
    organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="X"
/clone="RP23-335N15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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100.0%; Pic
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                               1 (bases 1 to 177264)
Phillimore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: UK-MRC
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                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECTOR: pBACe3.6
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Best Local Similarity
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AC094221/c
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KEYWORDS
                                                                                                              JOURNAL
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                                                                                                                                                                                           COMMENT
                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                             /note="match: EXTS: Em., All 13649.1 Em:AI798535.1
Em:AU142843.1 Em:BG196826.1 Em:BG327641.1 Em:BI551191.1
Em:AU142843.1 Em:BG196826.1 Em:BG327641.1 Em:BI551191.1
Em:CA488835.1 Em:EB130475.1 Em:CB218437.1 Em:CD516142.1
Em:CD520159.1 Em:EA1323.1
match: cDNAs: Em:AK024006.1"
complement (join(26256. .26481,50156. .50304,51096. .51173, jene="EIF2B3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (26256. .26481,50156. .50304,51096. .51173, .25296. .55486,57090. .57217,72833. .72922,102106. .>102133))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL626782 177264 bp DNA linear ROD 29-JUN-2002
Mouse DNA sequence from clone RP23-335N15 on chromosome X, complete
sequence.
                                                                         /locus_tag="RP5-88207.2-001"
complement(join(26256. .26481.33182. .33285,50156. .50304,
21096. .51173,55296. .55486,57090. .57217,72833. .72922,
102106. .102217,116984. .117143,153793. .153938,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Jocus_tag="RP5-88207.2-008"
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151096. .5173,55296. .55486,57090. .57217,72833. .72922,
102106. .102217,116984. .117143,153793. .153938,
156499. .156646))
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/translation="MEFQAVVMAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLE"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                            /locus tag="RP5-88207.2-001"
/product="eukaryotic translation initiation factor 2B,
subunit 3 gamma, 58kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="eukaryotic translation initiation factor 2B, subunit 3 gamma, 58KDa" /note="match: ESTs: Em:A1937500.1 Em:BG744900.1" complement(26318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
'product="eukaryotic_translation initiation factor 2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="match: proteins: Sw:P70541 Sw:Q9NR50 Tr:Q7ZTY5
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102106. .102217,116984. .117143,153793. .153938,
156499. .156655,161971. .162088))
/gene="EIF2B3"
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standard name="OTTHUMP00000010262"
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100.0%; Pred. No. 3.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="RP5-88207.2-008"
complement(26336..26341)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subunit 3 gamma, 58kDa"
/protein id="CAI23131.1"
/db_xref="GI:56204907"
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                                                                                                                                                                                                                  gene="EIF2B3'
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Marches 19, Conservative
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Gaps

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Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Grant, N., Marky, C., Bruch, P., Banch, K., Galleron, E., Chardon, J., Chanca, D., Durbin, K., Duyal, B., Bare, M., Dayal, M., Martial, M., Mart
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Sciulogiaturi, multipued; multipued; martine; martine; martine; martine; multipued; mult
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas;
Consensus quality: 209974 bases at least Q40
Consensus quality: 211630 bases at least Q30
Consensus quality: 212387 bases at least Q20
Estimated insert size: 224886; sum-of-contigs estimation
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
1. .215043
/organism="Rattus norvegicus"
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/estimated_length=unknown
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/db_xref="taxon:10116"
/clone="CH230-2P14"
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Matches 19; Conservative
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Direct Submission

AL Submitted (14-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Say (bases 1 to 225692)

Sat Genome Sequencing Consortium.

Direct Submission

AL Submitted (19-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:22772437.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P. Fraser, C.M., Gabisi, A., Ganta, R., Gardy, M., Garra, M., Gebregeorgis, S., Finley, M., Flagg, N., Gardy, M., Garra, M., Guarather, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, R., Hanse, S., Haddun, S.L., Hodgson, A., Hogues, M., Hellins, B., Howell, P., Handen, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idhebird, D., Jackson, A., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Lewis, L., Liu, Y., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., Loulseged, H., Lozan, J., Lewis, L., Liu, Z., Liu, W., Mahindarte, M., Martin, R., Moris, S., Muloavije, C., Neal, D., Nevton, N., Nguyen, N., Noris, S., Parks, K., Plopper, F., Poindexter, A., Poerz, L., Pera, L. L., Plopper, R., Poindexter, A., Poerz, L., Pera, L. L., Plopper, R., Poindexter, A., Poerz, L., Pera, R., Reder, R., Reder, R., Savers, R., Tabor, P., Taylor, C., Taylor, R., Waright, D., Waright, R., Wu, S., Van, R., Warren, J., Warren, J., Warren, J., Warren, J., Warren, S., Van, R., Savers, R., Weiss, R., Warren, Y., Warren, J., Warren, J., Warren, J., Yoon, V., Warren, S., Yand,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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AUTHORS TITLE JOURNAL

COMMENT

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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL A. 78.

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Rattús norvegicus clone CH230-62C14, *** SEQUENCING IN PROGRESS A:*, 6 unordered pieces.
                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                        Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Consensus quality: 212691 bases at least Q40
Consensus quality: 215052 bases at least Q30
Consensus quality: 215093 bases at least Q30
Estimated insert size: 223398; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                     218918: contig of 218818 bp in length 218918: gap of unknown length 220130: contig of 1212 bp in length 220230: gap of unknown length 221911: contig of 1681 bp in length 222011: gap of unknown length 2225354: contig of 1523 bp in length 2225344: gap of unknown length 2225344: gap of unknown length 222692: contig of 2058 bp in length.
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HTG; HTGS PHASEL; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)

    .225692
    /organism="Rattus norvegicus"

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estimated_length=unknown
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/estimated_length=unknown
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/estimated_length=unknown
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/db_xref="taxon:10116"
/clone="CH230-4F4"
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115825. .117279
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218819. .218918
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/note="clone_boundary
clone_end:Sp6
site:EcoRI
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complement 7216935...2.
/note="clone_boundary
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Best Local Similarity 100.0
Matches 19; Conservative
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20568 IGAATATATATACAAAGC 20550
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                                                                                 Schlunggarnin, muroncas, muridas, murinas, matchs, schlunggarnin, muroncas, murinas, matchs, schlossy, sch
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Submitted (19-JUL-2002) Human Genome Sequencing Center, Departmer
Submitted (19-JUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 281699)
Rat Genome Sequencing Consortium.
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COMMENT

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and separated
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individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole shorgun sequence reads. Both end sequences and whole shorgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrapy version 0.990329
Assembly program: Phrapy version 0.990329
Consensus quality: 235016 bases at least Q40
Consensus quality: 239978 bases at least Q30
Consensus quality: 242716 bases at least Q30
Consensus quality: 242716 bases at least Q30
Estimated insert size: 24569; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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8544 261385: contig of 252842 bp in length
186 261485: gap of unknown length
1486 262787: contig of 1302 bp in length
1788 26287: contig of 1302 bp in length
1788 26287: contig of 1302 bp in length
1788 265041: contig of 2127 bp in length
1788 265041: contig of 2127 bp in length
1788 26869: contig of 2127 bp in length
1788 26869: contig of 21730 bp in length
18870 281699: contig of 12730 bp in length
1870 281699: contig of 12730 bp in length
1870 281699: contig of 12730 bp in length
18870 281699: contig of 12730 bp in length
18870 281699: contig of 12730 bp in length.
                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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8544. .9701
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262788. .262887
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/estimated_length=unknown
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259995. .261385
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261386. .261485
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Matches 19; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

DEFINITION

ACCESSION

RESULT 14 BV373314

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FEATURES
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                                                                            BV373314 59-JAN-2005 S231P6596FC11.T0 BedlingtonTerrier Canis familiaris STS genomic,
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A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defined as mismatch positions that had a base quality of >= 30 on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which the particular read came. The validation rate for these SNPs was estimated at approximately 98*. WGA-discovery (WGA) of Boxer/Poodle SNPs:
A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WGS reads were placed uniquely on the CanFaml.0 boxer assembly and SNP detection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paired-end low-coverage whole genome shotgun reads were generated from 9 breeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotated with alleles from the boxer and the breed or canid from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retriever, English
Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
Water Dog -100,000 each)
and five other canids (Chinese, Alaskan, Indian and Spanish Gray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poddle sequence was placed uniquely on the CanFaml.0 boxer assembly and SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotated with alleles between the two boxer alleles. The validation rate for these SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The genome sequence of Canis familiaris Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 592
Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerstin Lindblad-Toh
                                                                                                                                                                                                BV373314.1 GI:57627384
                                                                                                                                                                                                                                                    Canis familiaris (dog)
Canis familiaris
                                                                                                                                         sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGS-discovery (WGS):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolf as well as the
Californian Coyote).
                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 6172521477
                                                                                                                                                                                                                                                                                                                                                                                                                            Lindblad-Toh, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research
                                                                                                                                                                                                                                                                                                                                                                              Canis.
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A Company of the Company of the Company " Water street man

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(Gon, Unknown Ching). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500p in length, at least 50% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNOS(30,25) (single strand NQS, the SNOS(30,25) (single strand NQS, the base in question has Phred score >= 30, the surrounding 10 bases in the read have Phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BV595271 606 bp DNA linear STS 14-APR-2005
S215P61223RG4.T0 Clara Pan troglodytes troglodytes STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 606)
Mikkelgen, T.S., Hillier, W.L., Bichler, E.E., Zody, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI
Build 34 (hgl6,July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score >= 25), and the read must have at least 200 bp SNQS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                       Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                       /mol_type="genomic DNA"
/strain="BedlingtonTerrier"
/db_xref="taxon:9615"
/map="+2 72-544 38436142-38435620"
/clone lib="BedlingtonTerrier"
<1. .>592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
                                                                                                                                                                                                                                                                                                                                                 92.0%; Score 18.4; DB 10; 95.0%; Pred. No. 4.9e+03; ive 0; Mismatches 1;
                                                                                  organism="Canis familiaris"
was estimated at approximately TBD%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Michael C. Zody
Broad Institute of MIT and Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 606
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 TTGAATCTATATTACAAAGC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAATATATATACAAAGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BV595271.1 GI:62534185
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.0%,
-hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of unknown origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol:
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discarded. After above filtering, NQS (30,25) standard was applied to all pairs of overlapping reads to call NQS bases and SNPs. Alignments (between two reads) with less than 100 NQS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share stingle read, comparisons between two reads that share solved a single read, comparisons between two reads that share slignments (>=95% bases of read A and >=95% bases of read B were placed at the same locus of human genome) were discarded.

Location/Qualifiers

1. 606

And_type="genomic DNA"

| Mub_species="troglodytes"
| Ab_refe="genomic DNA"
| Clone_lib="clara"
| Clone_lib="clara"
| Clone_lib="clara"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.0%; Score 18.4; DB 10; Length 606; Best Local Similarity 95.0%; Pred. No. 4.9e+03; Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TIGAATATATATACAAAGC 20
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ORIGIN
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Search completed: March 31, 2006, 12:41:31 Job time : 104.926 secs

77 TTCAATATATATTACAAAGC 96

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